



SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANTS: Sharpe, Sharpe
 Borriello, Francescopaolo
 Freeman, Gordon
 Nadler, Lee

(ii) TITLE OF INVENTION: Novel Forms of T Cell Costimulatory Molecules
 and Uses Therefor

(iii) NUMBER OF SEQUENCES: 65

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: LAHIVE & COCKFIELD
 (B) STREET: 28 State Street
 (C) CITY: Boston
 (D) STATE: Massachusetts
 (E) COUNTRY: USA
 (F) ZIP: 02109-1875

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
 (B) COMPUTER: IBM PC compatible
 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 (D) SOFTWARE: ASCII Text

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:
 (B) FILING DATE:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/205,697
 (B) FILING DATE: 02-Mar-1994

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Mandragouras, Amy E.
 (B) REGISTRATION NUMBER: 36,207
 (C) REFERENCE/DOCKET NUMBER: BWI-120CPUS

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (617)227-7400
 (B) TELEFAX: (617)227-5941

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1888 base pairs

46

A

(B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS
 (B) LOCATION: 249..1208

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GAGTTTATA CCTCAATAGA CTCTTACTAG TTTCTCTTTT TCAGGTTGTG AAACCTCAACC 60
 TTCAAAGACA CTCTGTTCCA TTTCTGTGGA CTAATAGGAT CATCTTTAGC ATCTGCCGGG 120
 TGGATGCCAT CCAGGCTTCT TTTTCTACAT CTCTGTTTCT CGATTTTTGT GAGCCTAGGA 180
 GGTGCCTAAG CTCCATTGGC TCTAGATTCC TGGCTTTCCC CATCATGTTC TCCAAAGCAT 240
 CTGAAGCT ATG GCT TGC AAT TGT CAG TTG ATG CAG GAT ACA CCA CTC CTC 290
 Met Ala Cys Asn Cys Gln Leu Met Gln Asp Thr Pro Leu Leu
 1 5 10
 AAG TTT CCA TGT CCA AGG CTC AAT CTT CTC TTT GTG CTG CTG ATT CGT 338
 Lys Phe Pro Cys Pro Arg Leu Asn Leu Leu Phe Val Leu Leu Ile Arg
 15 20 25 30
 CTT TCA CAA GTG TCT TCA GAT GTT GAT GAA CAA CTG TCC AAG TCA GTG 386
 Leu Ser Gln Val Ser Ser Asp Val Asp Glu Gln Leu Ser Lys Ser Val
 35 40 45
 AAA GAT AAG GTA TTG CTG CCT TGC CGT TAC AAC TCT CCT CAT GAA GAT 434
 Lys Asp Lys Val Leu Leu Pro Cys Arg Tyr Asn Ser Pro His Glu Asp
 50 55 60
 GAG TCT GAA GAC CGA ATC TAC TGG CAA AAA CAT GAC AAA GTG GTG CTG 482
 Glu Ser Glu Asp Arg Ile Tyr Trp Gln Lys His Asp Lys Val Val Leu
 65 70 75
 TCT GTC ATT GCT GGG AAA CTA AAA GTG TGG CCC GAG TAT AAG AAC CGG 530
 Ser Val Ile Ala Gly Lys Leu Lys Val Trp Pro Glu Tyr Lys Asn Arg
 80 85 90
 ACT TTA TAT GAC AAC ACT ACC TAC TCT CTT ATC ATC CTG GGC CTG GTC 578
 Thr Leu Tyr Asp Asn Thr Thr Tyr Ser Leu Ile Ile Leu Gly Leu Val
 95 100 105 110
 CTT TCA GAC CGG GGC ACA TAC AGC TGT GTC GTT CAA AAG AAG GAA AGA 626
 Leu Ser Asp Arg Gly Thr Tyr Ser Cys Val Val Gln Lys Lys Glu Arg
 115 120 125
 GGA ACG TAT GAA GTT AAA CAC TTG GCT TTA GTA AAG TTG TCC ATC AAA 674
 Gly Thr Tyr Glu Val Lys His Leu Ala Leu Val Lys Leu Ser Ile Lys
 130 135 140

GCT GAC TTC TCT ACC CCC AAC ATA ACT GAG TCT GGA AAC CCA TCT GCA 722
 Ala Asp Phe Ser Thr Pro Asn Ile Thr Glu Ser Gly Asn Pro Ser Ala
 145 150 155

GAC ACT AAA AGG ATT ACC TGC TTT GCT TCC GGG GGT TTC CCA AAG CCT 770
 Asp Thr Lys Arg Ile Thr Cys Phe Ala Ser Gly Gly Phe Pro Lys Pro
 160 165 170

CGC TTC TCT TGG TTG GAA AAT GGA AGA GAA TTA CCT GGC ATC AAT ACG 818
 Arg Phe Ser Trp Leu Glu Asn Gly Arg Glu Leu Pro Gly Ile Asn Thr
 175 180 185 190

ACA ATT TCC CAG GAT CCT GAA TCT GAA TTG TAC ACC ATT AGT AGC CAA 866
 Thr Ile Ser Gln Asp Pro Glu Ser Glu Leu Tyr Thr Ile Ser Ser Gln
 195 200 205

CTA GAT TTC AAT ACG ACT CGC AAC CAC ACC ATT AAG TGT CTC ATT AAA 914
 Leu Asp Phe Asn Thr Thr Arg Asn His Thr Ile Lys Cys Leu Ile Lys
 210 215 220

TAT GGA GAT GCT CAC GTG TCA GAG GAC TTC ACC TGG GAA AAA CCC CCA 962
 Tyr Gly Asp Ala His Val Ser Glu Asp Phe Thr Trp Glu Lys Pro Pro
 225 230 235

GAA GAC CCT CCT GAT AGC AAG AAC ACA CTT GTG CTC TTT GGG GCA GGA 1010
 Glu Asp Pro Pro Asp Ser Lys Asn Thr Leu Val Leu Phe Gly Ala Gly
 240 245 250

TTC GGC GCA GTA ATA ACA GTC GTC GTC ATC GTT GTC ATC ATC AAA TGC 1058
 Phe Gly Ala Val Ile Thr Val Val Val Ile Val Val Ile Ile Lys Cys
 255 260 265 270

TTC TGT AAG CAC GGT CTC ATC TAC CAT TTG CAA CTG ACC TCT TCT GCA 1106
 Phe Cys Lys His Gly Leu Ile Tyr His Leu Gln Leu Thr Ser Ser Ala
 275 280 285

AAG GAC TTC AGA AAC CTA GCA CTA CCC TGG CTC TGC AAA CAC GGT TCT 1154
 Lys Asp Phe Arg Asn Leu Ala Leu Pro Trp Leu Cys Lys His Gly Ser
 290 295 300

CTA GGT GAA GCC TCT GCA GTG ATT TGC AGA AGT ACT CAG ACG AAT GAA 1202
 Leu Gly Glu Ala Ser Ala Val Ile Cys Arg Ser Thr Gln Thr Asn Glu
 305 310 315

CCA CAG TAGTTCTGCT GTTTCTGAGG ACGTAGTTTA GAGACTGAAT TCTTTGGAAA 1258
 Pro Gln
 320

GGACATAGGG ACAGTTTGCA CATTTGCTTG CACATCACAC ACACACACAC ACACACACAC 1318

ACACACACAC ACACACACAC ACACACACAC ACACACACAC TCTCTCTCTC TCTCTCTCTC 1378

GATACCTTAG GATAGGGTTC TACCCTGTTG CTCAGTGACA AAGAATCACT CTGTGGCGGA 1438

GGCAGGCTTC AAGCTTGCAG CAATCCTCCT GCACCAGTTT CCTGAGTGCC AGACTTCCAG 1498

GTGTAAGCTA TGGCACTTAG CAGAACAATA GCTGAATCAA TGAAGACACT GAGGTTCCAA 1558

GAGGGAACCT GAATTATGAA GGTGAGTCAG AATCCAGATT TCCTGGCTCT ACCACTCTTA 1618

ACCTGTATCT GTTAGACCCC AAGCTCTGAG CTCATAGACA AGCTAATTTA AAATGCTTTT 1678
 TAATAAGCAG AAGGCTCAGT TAGTACGGGG TTCAGGATAC TGCTTACTGG CAATATTTGA 1738
 CTAGCCTCTA TTTTGTTTGT TTTTTAAAGG CCTACTGACT GTAGTGTAAT TTGTAGGAAA 1798
 CATGTTGCTA TGTATACCCA TTTGAGGGTA ATAAAAATGT TGGTAATTTT CAGCCAGCAC 1858
 TTTCCAGGTA TTTCCCTTTT TATCCTTCAT 1888

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 320 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Ala Cys Asn Cys Gln Leu Met Gln Asp Thr Pro Leu Leu Lys Phe
 1 5 10 15
 Pro Cys Pro Arg Leu Asn Leu Leu Phe Val Leu Leu Ile Arg Leu Ser
 20 25 30
 Gln Val Ser Ser Asp Val Asp Glu Gln Leu Ser Lys Ser Val Lys Asp
 35 40 45
 Lys Val Leu Leu Pro Cys Arg Tyr Asn Ser Pro His Glu Asp Glu Ser
 50 55 60
 Glu Asp Arg Ile Tyr Trp Gln Lys His Asp Lys Val Val Leu Ser Val
 65 70 75 80
 Ile Ala Gly Lys Leu Lys Val Trp Pro Glu Tyr Lys Asn Arg Thr Leu
 85 90 95
 Tyr Asp Asn Thr Thr Tyr Ser Leu Ile Ile Leu Gly Leu Val Leu Ser
 100 105 110
 Asp Arg Gly Thr Tyr Ser Cys Val Val Gln Lys Lys Glu Arg Gly Thr
 115 120 125
 Tyr Glu Val Lys His Leu Ala Leu Val Lys Leu Ser Ile Lys Ala Asp
 130 135 140
 Phe Ser Thr Pro Asn Ile Thr Glu Ser Gly Asn Pro Ser Ala Asp Thr
 145 150 155 160
 Lys Arg Ile Thr Cys Phe Ala Ser Gly Gly Phe Pro Lys Pro Arg Phe
 165 170 175
 Ser Trp Leu Glu Asn Gly Arg Glu Leu Pro Gly Ile Asn Thr Thr Ile
 180 185 190

Ser Gln Asp Pro Glu Ser Glu Leu Tyr Thr Ile Ser Ser Gln Leu Asp
195 200 205

Phe Asn Thr Thr Arg Asn His Thr Ile Lys Cys Leu Ile Lys Tyr Gly
210 215 220

Asp Ala His Val Ser Glu Asp Phe Thr Trp Glu Lys Pro Pro Glu Asp
225 230 235 240

Pro Pro Asp Ser Lys Asn Thr Leu Val Leu Phe Gly Ala Gly Phe Gly
245 250 255

Ala Val Ile Thr Val Val Val Ile Val Val Ile Ile Lys Cys Phe Cys
260 265 270

Lys His Gly Leu Ile Tyr His Leu Gln Leu Thr Ser Ser Ala Lys Asp
275 280 285

Phe Arg Asn Leu Ala Leu Pro Trp Leu Cys Lys His Gly Ser Leu Gly
290 295 300

Glu Ala Ser Ala Val Ile Cys Arg Ser Thr Gln Thr Asn Glu Pro Gln
305 310 315 320

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2516 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 249..1166

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GAGTTTTATA CCTCAATAGA CTCTTACTAG TTTCTCTTTT TCAGGTTGTG AAACCTCAACC 60
TTCAAAGACA CTCTGTTCCA TTTCTGTGGA CTAATAGGAT CATCTTTAGC ATCTGCCGGG 120
TGGATGCCAT CCAGGCTTCT TTTTCTACAT CTCTGTTTCT CGATTTTTGT GAGCCTAGGA 180
GGTGCCTAAG CTCCATTGGC TCTAGATTCC TGGCTTTCCC CATCATGTTC TCCAAAGCAT 240
CTGAAGCT ATG GCT TGC AAT TGT CAG TTG ATG CAG GAT ACA CCA CTC CTC 290
Met Ala Cys Asn Cys Gln Leu Met Gln Asp Thr Pro Leu Leu
1 5 10
AAG TTT CCA TGT CCA AGG CTC AAT CTT CTC TTT GTG CTG CTG AAT CGT 338
Lys Phe Pro Cys Pro Arg Leu Asn Leu Leu Phe Val Leu Leu Asn Arg
15 20 25 30

50

A

CTT TCA CAA GTG TCT TCA GAT GTT GAT GAA CAA CTG TCC AAG TCA GTG	386
Leu Ser Gln Val Ser Ser Asp Val Asp Glu Gln Leu Ser Lys Ser Val	
35 40 45	
AAA GAT AAG GTA TTG CTG CCT TGC CGT TAC AAC TCT CCT CAT GAA GAT	434
Lys Asp Lys Val Leu Leu Pro Cys Arg Tyr Asn Ser Pro His Glu Asp	
50 55 60	
GAG TCT GAA GAC CGA ATC TAC TGG CAA AAA CAT GAC AAA GTG GTG CTG	482
Glu Ser Glu Asp Arg Ile Tyr Trp Gln Lys His Asp Lys Val Val Leu	
65 70 75	
TCT GTC ATT GCT GGG AAA CTA AAA GTG TGG CCC GAG TAT AAG AAC CGG	530
Ser Val Ile Ala Gly Lys Leu Lys Val Trp Pro Glu Tyr Lys Asn Arg	
80 85 90	
ACT TTA TAT GAC AAC ACT ACC TAC TCT CTT ATC ATC CTG GGC CTG GTC	578
Thr Leu Tyr Asp Asn Thr Thr Tyr Ser Leu Ile Ile Leu Gly Leu Val	
95 100 105 110	
CTT TCA GAC CGG GGC ACA TAC AGC TGT GTC GTT CAA AAG AAG GAA AGA	626
Leu Ser Asp Arg Gly Thr Tyr Ser Cys Val Val Gln Lys Lys Glu Arg	
115 120 125	
GGA ACG TAT GAA GTT AAA CAC TTG GCT TTA GTA AAG TTG TCC ATC AAA	674
Gly Thr Tyr Glu Val Lys His Leu Ala Leu Val Lys Leu Ser Ile Lys	
130 135 140	
GCT GAC TTC TCT ACC CCC AAC ATA ACT GAG TCT GGA AAC CCA TCT GCA	722
Ala Asp Phe Ser Thr Pro Asn Ile Thr Glu Ser Gly Asn Pro Ser Ala	
145 150 155	
GAC ACT AAA AGG ATT ACC TGC TTT GCT TCC GGG GGT TTC CCA AAG CCT	770
Asp Thr Lys Arg Ile Thr Cys Phe Ala Ser Gly Gly Phe Pro Lys Pro	
160 165 170	
CGC TTC TCT TGG TTG GAA AAT GGA AGA GAA TTA CCT GGC ATC AAT ACG	818
Arg Phe Ser Trp Leu Glu Asn Gly Arg Glu Leu Pro Gly Ile Asn Thr	
175 180 185 190	
ACA ATT TCC CAG GAT CCT GAA TCT GAA TTG TAC ACC ATT AGT AGC CAA	866
Thr Ile Ser Gln Asp Pro Glu Ser Glu Leu Tyr Thr Ile Ser Ser Gln	
195 200 205	
CTA GAT TTC AAT ACG ACT CGC AAC CAC ACC ATT AAG TGT CTC ATT AAA	914
Leu Asp Phe Asn Thr Thr Arg Asn His Thr Ile Lys Cys Leu Ile Lys	
210 215 220	
TAT GGA GAT GCT CAC GTG TCA GAG GAC TTC ACC TGG GAA AAA CCC CCA	962
Tyr Gly Asp Ala His Val Ser Glu Asp Phe Thr Trp Glu Lys Pro Pro	
225 230 235	
GAA GAC CCT CCT GAT AGC AAG AAC ACA CTT GTG CTC TTT GGG GCA GGA	1010
Glu Asp Pro Pro Asp Ser Lys Asn Thr Leu Val Leu Phe Gly Ala Gly	
240 245 250	
TTC GGC GCA GTA ATA ACA GTC GTC GTC ATC GTT GTC ATC ATC AAA TGC	1058

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 818 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 1..138

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GGT CTC ATC TAC CAT TTG CAA CTG ACC TCT TCT GCA AAG GAC TTC AGA	48
Gly Leu Ile Tyr His Leu Gln Leu Thr Ser Ser Ala Lys Asp Phe Arg	
1 5 10 15	
AAC CTA GCA CTA CCC TGG CTC TGC AAA CAC GGT TCT CTA GGT GAA GCC	96
Asn Leu Ala Leu Pro Trp Leu Cys Lys His Gly Ser Leu Gly Glu Ala	
20 25 30	
TCT GCA GTG ATT TGC AGA AGT ACT CAG ACG AAT GAA CCA CAG	138
Ser Ala Val Ile Cys Arg Ser Thr Gln Thr Asn Glu Pro Gln	
35 40 45	
TAGTTCTGCT GTTTCTGAGG ACGTAGTTTA GAGACTGAAT TCTTTGGAAA GGACATAGGG	198
ACAGTTTGC AATTTGCTTG CACATCACAC ACACACACAC ACACACACAC ACACACACAC	258
ACACACACAC ACACACACAC ACACACACAC TCTCTCTCTC TCTCTCTCTC GATACCTTAG	318
GATAGGGTTC TACCCTGTTG CTCAGTGACA AAGAATCACT CTGTGGCGGA GGCAGGCTTC	378
AAGCTTGCAG CAATCCTCCT GCACCACTTT CCTGAGTGCC AGACTTCCAG GTGTAAGCTA	438
TGGCACTTAG CAGAACAATA GCTGAATCAA TGAAGACACT GAGGTTCCTA GAGGGAACCT	498
GAATTATGAA GGTGAGTCAG AATCCAGATT TCCTGGCTCT ACCACTCTTA ACCTGTATCT	558
GTTAGACCCC AAGCTCTGAG CTCATAGACA AGCTAATTTA AAATGCTTTT TAATAAGCAG	618
AAGGCTCAGT TAGTACGGGG TTCAGGATAC TGCTTACTGG CAATATTTGA CTAGCCTCTA	678
TTTTGTTTGT TTTTAAAGG CCTACTGACT GTAGTGTAAT TTGTAGGAAA CATGTTGCTA	738
TGTATACCCA TTTGAGGGTA ATAAAAATGT TGTAATTTT CAGCCAGCAC TTTCCAGGTA	798
TTTCCCTTTT TATCCTTCAT	818

(2) INFORMATION FOR SEQ ID NO:5:

53

A

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Gly Leu Ile Tyr His Leu Gln Leu Thr Ser Ser Ala Lys Asp Phe Arg
 1 5 10 15

Asn Leu Ala Leu Pro Trp Leu Cys Lys His Gly Ser Leu Gly Glu Ala
 20 25 30

Ser Ala Val Ile Cys Arg Ser Thr Gln Thr Asn Glu Pro Gln
 35 40 45

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1753 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GTTTTAGTAA CCAGAGGCCG CAAGAAGAGA TCACTTGTAT ATACACGGGC CCCATCTTTT 60
 GCTTTTTAAG ACAAAGAAA AAGAATCTTC TTCAACAAGT AAGTAAATGC ATTTACTATT 120
 TATCATGCTA TGGGACACCT TAGTAGAACA CGCTATCTCC AGCCTTATCA TATGCATATT 180
 TTGTTGTTGT TGTTGTTGTT GTTGTTAAAG ACAGGGTCTC ATATATGCCA GGCTGGTCCC 240
 AAACCTTTCAG TGTAACCCAA GATAATCTGG AACTCCCGAC TCCTCTGCTC CCACCTCTCC 300
 AGTGCAAGGAC ACTGTTTATA CCGTGCTGGG GAATTGAACT CAGAGCACCC TGCATGTCAG 360
 CTAAGCATTG TACCGACCAA GTCCCATGCC CAGTCCCTAA CTCCCCAACT TCACTGCTTT 420
 TTAAACATAC ATACAATCAT AACTTGCCCT CAGAGCAGTC TCCTGGGGTC TCTTATTCTC 480
 AAGGCTGCGG CATTCCAACA CTGTTAGAAA AACACCATCA GGATTCTTTT GTGTTTCCTA 540
 GATGCAAACA TTTTGTAGG GCGAAGTTGA GGTTTTCTA ATCAAGAAAA TGCCGGTAAC 600
 AAGTCTCTTC AAGCTAACTG GTTGGCTAAG GGGTATCTCT CCAAAGAAG AGATCCACAT 660
 GTCAGGCCAG TTGTAGGCAT GATGTCAGGT CTCCCTCCCT TTCTTTCTTT CTTTCTTTT 720
 TTCTTTCTTT CTTTTTTTCT TTCTTTCTTA CTTTCTTACT TTCTTTCTTT TCTGTTTTTT 780

GGTTTTTCGA GACAGGGTTT CTTTGTATAG CCCTGGCTGT CCTGGAACTC GCTCTGTAGA	840
CCAGGCTGGC CTCGAACTCA GAAATCTGCC TCTGCCTTTA CCTCCTGAGT GCTGGGAATT	900
AAAGGTGTGC ACCACCATGC CCGGCTGGGA TGTCATTTCGT TTTCATTTCT CAATTTTGAT	960
ACTTTATGGA AGAAAAAAGA AAAGATAGAC AAGCCTCTTC ATGTAATACC CCATAGTCTC	1020
AATAAGTGGT GTTCGTAACG TGGCTTCTCT TTCCTTACCT TTTACTGGTA GATTCTCGG	1080
TTGATTGATG TCCCTGTAGG ACTTACTGGG TTTAAGATTC TTGGTTTCCT GTTTTAAGAT	1140
ATAAAGAAAC CATTTCTTAA CTAAAACACT GCCTTGGACA AATATACTTT TGGCAGTCAC	1200
TCTGTGTCCA GAATGGAATT TAAGCTTTCA TGGCCTAGCT GCTAGTGAAG GTTCTTTGCT	1260
TTTTTTTGGC TGTTGTATGT GAAATGGGGT TGGGTGGGAA CCACCTCACT GTGTTCTAGT	1320
GTTAGTCACC CCACCCCCGC AAGCAGAATC CTTTTACCCA GCTTTTTTCAC CCAGCTGTGC	1380
TCACCCGGTG CTCAGAACAG GCCTGGACAA GTCACCTCCC CTAGAGTTCT GGGGACCTTT	1440
GAGTTGCCCT CATGGCCACA CCCTGATTCA GAACTCTCAC TCTGTCGTAA GATAGAGCTA	1500
CTGGGGAGTT TTATACCTCA ATAGACTCTT ACTAGTTTCT CTTTTTCAGG TTGTGAAACT	1560
CAACCTTCAA AGACACTCTG TTCCATTTCT GTGGACTAAT AGGATCATCT TTAGCATCTG	1620
CCGGGTGGAT GCCATCCAGG CTTCTTTTTT TACATCTCTG TTTCTCGATT TTTGTGAGCC	1680
TAGGAGGTGC CTAAGCTCCA TTGGCTCTAG ATTCCTGGCT TTCCCATCA TGTTCTCCAA	1740
AGCATCTGAA GCT	1753

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 158 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

TGTCCAGGCA GAGCTAGTGG CTGCCCCTAG CGCTTCCTCT TCTTTGATAC CCCAAAGTCT	60
GAGTTTATTA CACATCCTTG GTGACCAAAT CACATGGGAG CTCCTCCGA GGTCTTAGTA	120
AAGGGAAGTT GGAAAGGGGA AATTCCTGCC CCCCTGCC	158

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1398 base pairs

(B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS
 (B) LOCATION: 249..848

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GAGTTTTATA CCTCAATAGA CTCTTACTAG TTTCTCTTTT TCAGGTTGTG AAACCTCAACC	60
TTCAAAGACA CTCTGTTCCA TTTCTGTGGA CTAATAGGAT CATCTTTAGC ATCTGCCGGG	120
TGGATGCCAT CCAGGCTTCT TTTTCTACAT CTCTGTTTCT CGATTTTGTG GAGCCTAGGA	180
GGTGCCTAAG CTCCATTGGC TCTAGATTCC TGGCTTTCCC CATCATGTTT TCCAAAGCAT	240
CTGAAGCT ATG GCT TGC AAT TGT CAG TTG ATG CAG GAT ACA CCA CTC CTC	290
Met Ala Cys Asn Cys Gln Leu Met Gln Asp Thr Pro Leu Leu	
1 5 10	
AAG TTT CCA TGT CCA AGG CTC AAT CTT CTC TTT GTG CTG CTG ATT CGT	338
Lys Phe Pro Cys Pro Arg Leu Asn Leu Leu Phe Val Leu Leu Ile Arg	
15 20 25 30	
CTT TCA CAA GTG TCT TCA GCT GAC TTC TCT ACC CCC AAC ATA ACT GAG	386
Leu Ser Gln Val Ser Ser Ala Asp Phe Ser Thr Pro Asn Ile Thr Glu	
35 40 45	
TCT GGA AAC CCA TCT GCA GAC ACT AAA AGG ATT ACC TGC TTT GCT TCC	434
Ser Gly Asn Pro Ser Ala Asp Thr Lys Arg Ile Thr Cys Phe Ala Ser	
50 55 60	
GGG GGT TTC CCA AAG CCT CGC TTC TCT TGG TGG GAA AAT GGA AGA GAA	482
Gly Gly Phe Pro Lys Pro Arg Phe Ser Trp Trp Glu Asn Gly Arg Glu	
65 70 75	
TTA CCT GGC ATC AAT ACG ACA ATT TCC CAG GAT CCT GAA TCT GAA TTG	530
Leu Pro Gly Ile Asn Thr Thr Ile Ser Gln Asp Pro Glu Ser Glu Leu	
80 85 90	
TAC ACC ATT AGT AGC CAA CTA GAT TTC AAT ACG ACT CGC AAC CAC ACC	578
Tyr Thr Ile Ser Ser Gln Leu Asp Phe Asn Thr Thr Arg Asn His Thr	
95 100 105 110	
ATT AAG TGT CTC ATT AAA TAT GGA GAT GCT CAC GTG TCA GAG GAC TTC	626
Ile Lys Cys Leu Ile Lys Tyr Gly Asp Ala His Val Ser Glu Asp Phe	
115 120 125	
ACC TGG GAA AAA CCC CCA GAA GAC CCT CCT GAT AGC AAG AAC ACA CTT	674
Thr Trp Glu Lys Pro Pro Glu Asp Pro Pro Asp Ser Lys Asn Thr Leu	
130 135 140	
GTG CTC TTT GGG GCA GGA TTC GGC GCA GTA ATA ACA GTC GTC GTC ATC	722

Val	Leu	Phe	Gly	Ala	Gly	Phe	Gly	Ala	Val	Ile	Thr	Val	Val	Val	Ile		
	145						150					155					
GTT	GTC	ATC	ATC	AAA	TGC	TTC	TGT	AAG	CAC	AGA	AGC	TGT	TTC	AGA	AGA	770	
Val	Val	Ile	Ile	Lys	Cys	Phe	Cys	Lys	His	Arg	Ser	Cys	Phe	Arg	Arg		
	160					165					170						
AAT	GAG	GCA	AGC	AGA	GAA	ACA	AAC	AAC	AGC	CTT	ACC	TTC	GGG	CCT	GAA	818	
Asn	Glu	Ala	Ser	Arg	Glu	Thr	Asn	Asn	Ser	Leu	Thr	Phe	Gly	Pro	Glu		
175					180					185				190			
GAA	GCA	TTA	GCT	GAA	CAG	ACC	GTC	TTC	CTT	TAGTTCTTCT	CTGTCCATGT					868	
Glu	Ala	Leu	Ala	Glu	Gln	Thr	Val	Phe	Leu								
				195					200								
GGG	A	T	A	C	A	T	A	T	A	T	G	T	G			928	
GAT	C	T	T	T	C	G	G		A	C	A	A	G	A	T	A	G
GAT	T	T	C	T	T	T	C		A	T	C	A	G	A	A	G	A
GA	A	G	T	G	G	A	A		G	G	T	G	A	G	C	C	C
TG	G	G	T	G	G	T	A		T	A	A	A	A	A	A	A	A
TG	G	G	T	G	G	T	A		T	A	A	A	A	A	A	A	A
GG	G	A	G	A	G	T	G		G	A	G	A	G	A	A	A	A
GG	G	A	G	A	G	T	G		G	A	G	A	G	A	A	A	A
GG	G	A	G	A	G	T	G		G	A	G	A	G	A	A	A	A
TAT	A	A	T	A	T	T											

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 200 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met	Ala	Cys	Asn	Cys	Gln	Leu	Met	Gln	Asp	Thr	Pro	Leu	Leu	Lys	Phe		
1				5					10					15			
Pro	Cys	Pro	Arg	Leu	Ile	Leu	Leu	Phe	Val	Leu	Leu	Ile	Arg	Leu	Ser		
			20					25					30				
Gln	Val	Ser	Ser	Ala	Asp	Phe	Ser	Thr	Pro	Asn	Ile	Thr	Glu	Ser	Gly		
		35					40					45					
Asn	Pro	Ser	Ala	Asp	Thr	Lys	Arg	Ile	Thr	Cys	Phe	Ala	Ser	Gly	Gly		
	50					55					60						
Phe	Pro	Lys	Pro	Arg	Phe	Ser	Trp	Leu	Glu	Asn	Gly	Arg	Glu	Leu	Pro		
65					70					75					80		

57

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Gly	Ile	Asn	Thr	Thr	Ile	Ser	Gln	Asp	Pro	Glu	Ser	Glu	Leu	Tyr	Thr
				85					90					95	
Ile	Ser	Ser	Gln	Leu	Asp	Phe	Asn	Thr	Thr	Arg	Asn	His	Thr	Ile	Lys
			100					105					110		
Cys	Leu	Ile	Lys	Tyr	Gly	Asp	Ala	His	Val	Ser	Glu	Asp	Phe	Thr	Trp
		115					120					125			
Glu	Lys	Pro	Pro	Glu	Asp	Pro	Pro	Asp	Ser	Lys	Asn	Thr	Leu	Val	Leu
	130					135					140				
Phe	Gly	Ala	Gly	Phe	Gly	Ala	Val	Ile	Thr	Val	Val	Val	Ile	Val	Val
145					150					155					160
Ile	Ile	Lys	Cys	Phe	Cys	Lys	His	Arg	Ser	Cys	Phe	Arg	Arg	Asn	Glu
				165					170					175	
Ala	Ser	Arg	Glu	Thr	Asn	Asn	Ser	Leu	Thr	Phe	Gly	Pro	Glu	Glu	Ala
			180					185					190		
Leu	Ala	Glu	Gln	Thr	Val	Phe	Leu								
		195					200								

(2) INFORMATION FOR SEO ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1570 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
(B) LOCATION: 249..890

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GAGT	TTTT	TATA	CCTC	AATAGA	CTCT	TACTAG	TTTCT	CTTTTT	TCAG	GTGTG	AAACT	CAACC	60			
TTCA	AAGACA	CTCT	GTTCCA	TTTCT	GTGGA	CTAAT	AGGAT	CATCT	TTTAGC	ATCT	GCCGGG	120				
TGGAT	GCCAT	CCAG	GCTTCT	TTTT	CTACAT	CTCT	GTTTCT	CGAT	TTTTTGT	GAGC	CTAGGA	180				
GGTGC	CCTAAG	CTCC	ATTGGC	TCTAG	ATTCC	TGGC	TTTCCC	CATCAT	GTTC	TCCAA	AGCAT	240				
CTGA	AGCT	ATG	GCT	TGC	AAT	TGT	CAG	TTG	ATG	CAG	GAT	ACA	CCA	CTC	CTC	290
	Met	Ala	Cys	Asn	Cys	Gln	Leu	Met	Gln	Asp	Thr	Pro	Leu	Leu		
	1				5					10						
AAG	TTT	CCA	TGT	CCA	AGG	CTC	AAT	CTT	CTC	TTT	GTG	CTG	CTG	ATT	CGT	338
Lys	Phe	Pro	Cys	Pro	Arg	Leu	Asn	Leu	Leu	Phe	Val	Leu	Leu	Ile	Arg	
	15				20					25				30		
CTT	TCA	CAA	GTG	TCT	TCA	GCT	GAC	TTC	TCT	ACC	CCC	AAC	ATA	ACT	GAG	386

Leu	Ser	Gln	Val	Ser	Ser	Ala	Asp	Phe	Ser	Thr	Pro	Asn	Ile	Thr	Glu	
				35					40						45	
TCT	GGA	AAC	CCA	TCT	GCA	GAC	ACT	AAA	AGG	ATT	ACC	TGC	TTT	GCT	TCC	434
Ser	Gly	Asn	Pro	Ser	Ala	Asp	Thr	Lys	Arg	Ile	Thr	Cys	Phe	Ala	Ser	
			50					55					60			
GGG	GGT	TTC	CCA	AAG	CCT	CGC	TTC	TCT	TGG	TTG	GAA	AAT	GGA	AGA	GAA	482
Gly	Gly	Phe	Pro	Lys	Pro	Arg	Phe	Ser	Trp	Leu	Glu	Asn	Gly	Arg	Glu	
		65					70					75				
TTA	CCT	GGC	ATC	AAT	ACG	ACA	ATT	TCC	CAG	GAT	CCT	GAA	TCT	GAA	TTG	530
Leu	Pro	Gly	Ile	Asn	Thr	Thr	Ile	Ser	Gln	Asp	Pro	Glu	Ser	Glu	Leu	
	80						85				90					
TAC	ACC	ATT	AGT	AGC	CAA	CTA	GAT	TTC	AAT	ACG	ACT	CGC	AAC	CAC	ACC	578
Tyr	Thr	Ile	Ser	Ser	Gln	Leu	Asp	Phe	Asn	Thr	Thr	Arg	Asn	His	Thr	
	95				100					105					110	
ATT	AAG	TGT	CTC	ATT	AAA	TAT	GGA	GAT	GCT	CAC	GTG	TCA	GAG	GAC	TTC	626
Ile	Lys	Cys	Leu	Ile	Lys	Tyr	Gly	Asp	Ala	His	Val	Ser	Glu	Asp	Phe	
				115					120					125		
ACC	TGG	GAA	AAA	CCC	CCA	GAA	GAC	CCT	CCT	GAT	AGC	AAG	AAC	ACA	CTT	674
Thr	Trp	Glu	Lys	Pro	Pro	Glu	Asp	Pro	Pro	Asp	Ser	Lys	Asn	Thr	Leu	
			130					135					140			
GTG	CTC	TTT	GGG	GCA	GGA	TTC	GGC	GCA	GTA	ATA	ACA	GTC	GTC	GTC	ATC	722
Val	Leu	Phe	Gly	Ala	Gly	Phe	Gly	Ala	Val	Ile	Thr	Val	Val	Val	Ile	
		145					150					155				
GTT	GTC	ATC	ATC	AAA	TGC	TTC	TGT	AAG	CAC	GGT	CTC	ATC	TAC	CAT	TTG	770
Val	Val	Ile	Ile	Lys	Cys	Phe	Cys	Lys	His	Gly	Leu	Ile	Tyr	His	Leu	
	160					165					170					
CAA	CTG	ACC	TCT	TCT	GCA	AAG	GAC	TTC	AGA	AAC	CTA	GCA	CTA	CCC	TGG	818
Gln	Leu	Thr	Ser	Ser	Ala	Lys	Asp	Phe	Arg	Asn	Leu	Ala	Leu	Pro	Trp	
	175				180					185					190	
CTC	TGC	AAA	CAC	GGT	TCT	CTA	GGT	GAA	GCC	TCT	GCA	GTG	ATT	TGC	AGA	866
Leu	Cys	Lys	His	Gly	Ser	Leu	Gly	Glu	Ala	Ser	Ala	Val	Ile	Cys	Arg	
				195				200					205			
AGT	ACT	CAG	ACG	AAT	GAA	CCA	CAG	TAGTTCTGCT	GTTTCTGAGG	ACGTAGTTTA						920
Ser	Thr	Gln	Thr	Asn	Glu	Pro	Gln									
				210												
GAGACTGAAT	TCTTTGGAAA	GGACATAGGG	ACAGTTTGCA	CATTTGCTTG	CACATCACAC											980
ACACACACAC	ACACACACAC	ACACACACAC	ACACACACAC	ACACACACAC	ACACACACAC											1040
TCTCTCTCTC	TCTCTCTCTC	GATACCTTAG	GATAGGGTTC	TACCCTGTTG	CTCAGTGACA											1100
AAGAATCACT	CTGTGGCGGA	GGCAGGCTTC	AAGCTTGCAG	CAATCCTCCT	GCACCAGTTT											1160
CCTGAGTGCC	AGACTTCCAG	GTGTAAGCTA	TGGCACTTAG	CAGAACACTA	GCTGAATCAA											1220
TGAAGACACT	GAGGTTCCAA	GAGGGAACCT	GAATTATGAA	GGTGAGTCAG	AATCCAGATT											1280

TCCTGGCTCT ACCACTCTTA ACCTGTATCT GTTAGACCCC AAGCTCTGAG CTCATAGACA 1340
 AGCTAATTTA AAATGCTTTT TAATAAGCAG AAGGCTCAGT TAGTACGGGG TTCAGGATAC 1400
 TGCTTACTGG CAATATTTGA CTAGCCTCTA TTTTGTTTGT TTTTAAAGG CCTACTGACT 1460
 GTAGTGTAAT TTGTAGGAAA CATGTTGCTA TGTATACCCA TTTGAGGGTA ATAAAAATGT 1520
 TGGTAATTTT CAGCCAGCAC TTTCCAGGTA TTTCCCTTTT TATCCTTCAT 1570

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 214 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met Ala Cys Asn Cys Gln Leu Met Gln Asp Thr Pro Leu Leu Lys Phe
 1 5 10 15
 Pro Cys Pro Arg Leu Ile Leu Leu Phe Val Leu Leu Ile Arg Leu Ser
 20 25 30
 Gln Val Ser Ser Ala Asp Phe Ser Thr Pro Asn Ile Thr Glu Ser Gly
 35 40 45
 Asn Pro Ser Ala Asp Thr Lys Arg Ile Thr Cys Phe Ala Ser Gly Gly
 50 55 60
 Phe Pro Lys Pro Arg Phe Ser Trp Leu Glu Asn Gly Arg Glu Leu Pro
 65 70 75 80
 Gly Ile Asn Thr Thr Ile Ser Gln Asp Pro Glu Ser Glu Leu Tyr Thr
 85 90 95
 Ile Ser Ser Gln Leu Asp Phe Asn Thr Thr Arg Asn His Thr Ile Lys
 100 105 110
 Cys Leu Ile Lys Tyr Gly Asp Ala His Val Ser Glu Asp Phe Thr Trp
 115 120 125
 Glu Lys Pro Pro Glu Asp Pro Pro Asp Ser Lys Asn Thr Leu Val Leu
 130 135 140
 Phe Gly Ala Gly Phe Gly Ala Val Ile Thr Val Val Val Ile Val Val
 145 150 155 160
 Ile Ile Lys Cys Phe Cys Lys His Gly Leu Ile Tyr His Leu Gln Leu
 165 170 175
 Thr Ser Ser Ala Lys Asp Phe Arg Asn Leu Ala Leu Pro Trp Leu Cys

60

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180	185	190
Lys His Gly Ser Leu Gly Glu Ala Ser Ala Val Ile Cys Arg Ser Thr		
195	200	205
Gln Thr Asn Glu Pro Gln		
210		

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1261 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 194..1135

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

AGNCCCNAGA TTATTTCTCC CTGTATAAGG GACGCCCAGG AGGCCTGGGG AGCGGACAAG	60
GCTCCTTTTA CTTTCTTCT TCTTCTATTT TTTTACCTT CTATTTTTTT CTTCATGTTC	120
CTGTGATCTT CGGGAATGCT GCTGTGCTTG TGTGTGTGGT CCCTGAGCGC CGAGGTGGAG	180
AGGCACTGGT GAC ATG TAT GTC ATC AAG ACA TGT GCA ACC TGC ACC ATG	229
Met Tyr Val Ile Lys Thr Cys Ala Thr Cys Thr Met	
1 5 10	
GGC TTG GCA ATC CTT ATC TTT GTG ACA GTC TTG CTG ATC TCA GAT GCT	277
Gly Leu Ala Ile Leu Ile Phe Val Thr Val Leu Leu Ile Ser Asp Ala	
15 20 25	
GTT TCC GTG GAG ACG CAA GCT TAT TTC AAT GGG ACT GCA TAT CTG CCG	325
Val Ser Val Glu Thr Gln Ala Tyr Phe Asn Gly Thr Ala Tyr Leu Pro	
30 35 40	
TGC CCA TTT ACA AAG GCT CAA AAC ATA AGC CTG AGT GAG CTG GTA GTA	373
Cys Pro Phe Thr Lys Ala Gln Asn Ile Ser Leu Ser Glu Leu Val Val	
45 50 55 60	
TTT TGG CAG GAC CAG CAA AAG TTG GTT CTG TAC GAG CAC TAT TTG GGC	421
Phe Trp Gln Asp Gln Gln Lys Leu Val Leu Tyr Glu His Tyr Leu Gly	
65 70 75	
ACA GAG AAA CTT GAT AGT GTG AAT GCC AAG TAC CTG GGC CGC ACG AGC	469
Thr Glu Lys Leu Asp Ser Val Asn Ala Lys Tyr Leu Gly Arg Thr Ser	
80 85 90	
TTT GAC AGG AAC AAC TGG ACT CTA CGA CTT CAC AAT GTT CAG ATC AAG	517

Phe	Asp	Arg	Asn	Asn	Trp	Thr	Leu	Arg	Leu	His	Asn	Val	Gln	Ile	Lys	
		95					100					105				
GAC	ATG	GGC	TCG	TAT	GAT	TGT	TTT	ATA	CAA	AAA	AAG	CCA	CCC	ACA	GGA	565
Asp	Met	Gly	Ser	Tyr	Asp	Cys	Phe	Ile	Gln	Lys	Lys	Pro	Pro	Thr	Gly	
	110					115					120					
TCA	ATT	ATC	CTC	CAA	CAG	ACA	TTA	ACA	GAA	CTG	TCA	GTG	ATC	GCC	AAC	613
Ser	Ile	Ile	Leu	Gln	Gln	Thr	Leu	Thr	Glu	Leu	Ser	Val	Ile	Ala	Asn	
125					130					135					140	
TTC	AGT	GAA	CCT	GAA	ATA	AAA	CTG	GCT	CAG	AAT	GTA	ACA	GGA	AAT	TCT	661
Phe	Ser	Glu	Pro	Glu	Ile	Lys	Leu	Ala	Gln	Asn	Val	Thr	Gly	Asn	Ser	
				145					150					155		
GGC	ATA	AAT	TTG	ACC	TGC	ACG	TCT	AAG	CAA	GGT	CAC	CCG	AAA	CCT	AAG	709
Gly	Ile	Asn	Leu	Thr	Cys	Thr	Ser	Lys	Gln	Gly	His	Pro	Lys	Pro	Lys	
			160					165						170		
AAG	ATG	TAT	TTT	CTG	ATA	ACT	AAT	TCA	ACT	AAT	GAG	TAT	GGT	GAT	AAC	757
Lys	Met	Tyr	Phe	Leu	Ile	Thr	Asn	Ser	Thr	Asn	Glu	Tyr	Gly	Asp	Asn	
		175					180					185				
ATG	CAG	ATA	TCA	CAA	GAT	AAT	GTC	ACA	GAA	CTG	TTC	AGT	ATC	TCC	AAC	805
Met	Gln	Ile	Ser	Gln	Asp	Asn	Val	Thr	Glu	Leu	Phe	Ser	Ile	Ser	Asn	
	190					195					200					
AGC	CTC	TCT	CTT	TCA	TTC	CCG	GAT	GGT	GTG	TGG	CAT	ATG	ACC	GTT	GTG	853
Ser	Leu	Ser	Leu	Ser	Phe	Pro	Asp	Gly	Val	Trp	His	Met	Thr	Val	Val	
205					210					215				220		
TGT	GTT	CTG	GAA	ACG	GAG	TCA	ATG	AAG	ATT	TCC	TCC	AAA	CCT	CTC	AAT	901
Cys	Val	Leu	Glu	Thr	Glu	Ser	Met	Lys	Ile	Ser	Ser	Lys	Pro	Leu	Asn	
				225					230					235		
TTC	ACT	CAA	GAG	TTT	CCA	TCT	CCT	CAA	ACG	TAT	TGG	AAG	GAG	ATT	ACA	949
Phe	Thr	Gln	Glu	Phe	Pro	Ser	Pro	Gln	Thr	Tyr	Trp	Lys	Glu	Ile	Thr	
			240					245					250			
GCT	TCA	GTT	ACT	GTG	GCC	CTC	CTC	CTT	GTG	ATG	CTG	CTC	ATC	ATT	GTA	997
Ala	Ser	Val	Thr	Val	Ala	Leu	Leu	Leu	Val	Met	Leu	Leu	Ile	Ile	Val	
		255				260						265				
TGT	CAC	AAG	AAG	CCG	AAT	CAG	CCT	AGC	AGG	CCC	AGC	AAC	ACA	GCC	TCT	1045
Cys	His	Lys	Lys	Pro	Asn	Gln	Pro	Ser	Arg	Pro	Ser	Asn	Thr	Ala	Ser	
	270					275					280					
AAG	TTA	GAG	CGG	GAT	AGT	AAC	GCT	GAC	AGA	GAG	ACT	ATC	AAC	CTG	AAG	1093
Lys	Leu	Glu	Arg	Asp	Ser	Asn	Ala	Asp	Arg	Glu	Thr	Ile	Asn	Leu	Lys	
285					290					295				300		
GAA	CTT	GAA	CCC	CAA	ATT	GCT	TCA	GCA	AAA	CCA	AAT	GCA	GAG			1135
Glu	Leu	Glu	Pro	Gln	Ile	Ala	Ser	Ala	Lys	Pro	Asn	Ala	Glu			
				305						310						
TGAAGGCAGT	GAGAGCCTGA	GGAAAGAGTT	AAAAATTGCT	TTGCCTGAAA	TAAGAAGTGC											1195

AGAGTTTCTC AGAATTCAAA AATGTTCTCA GCTGATTGGA ATTCTACAGT TGAATAATTA 1255
AAGAAC 1261

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 314 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

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Met Tyr Val Ile Lys Thr Cys Ala Thr Cys Thr Met Gly Leu Ala Ile
 1             5             10             15
Leu Ile Phe Val Thr Val Leu Leu Ile Ser Asp Ala Val Ser Val Glu
          20             25             30
Thr Gln Ala Tyr Phe Asn Gly Thr Ala Tyr Leu Pro Cys Pro Phe Thr
          35             40             45
Lys Ala Gln Asn Ile Ser Leu Ser Glu Leu Val Val Phe Trp Gln Asp
          50             55             60
Gln Gln Lys Leu Val Leu Tyr Glu His Tyr Leu Gly Thr Glu Lys Leu
          65             70             75             80
Asp Ser Val Asn Ala Lys Tyr Leu Gly Arg Thr Ser Phe Asp Arg Asn
          85             90             95
Asn Trp Thr Leu Arg Leu His Asn Val Gln Ile Lys Asp Met Gly Ser
          100            105            110
Tyr Asp Cys Phe Ile Gln Lys Lys Pro Pro Thr Gly Ser Ile Ile Leu
          115            120            125
Gln Gln Thr Leu Thr Glu Leu Ser Val Ile Ala Asn Phe Ser Glu Pro
          130            135            140
Glu Ile Lys Leu Ala Gln Asn Val Thr Gly Asn Ser Gly Ile Asn Leu
          145            150            155            160
Thr Cys Thr Ser Lys Gln Gly His Pro Lys Pro Lys Lys Met Tyr Phe
          165            170            175
Leu Ile Thr Asn Ser Thr Asn Glu Tyr Gly Asp Asn Met Gln Ile Ser
          180            185            190
Gln Asp Asn Val Thr Glu Leu Phe Ser Ile Ser Asn Ser Leu Ser Leu
          195            200            205
Ser Phe Pro Asp Gly Val Trp His Met Thr Val Val Cys Val Leu Glu
          210            215            220
Thr Glu Ser Met Lys Ile Ser Ser Lys Pro Leu Asn Phe Thr Gln Glu

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225		230		235		240									
Phe	Pro	Ser	Pro	Gln	Thr	Tyr	Trp	Lys	Glu	Ile	Thr	Ala	Ser	Val	Thr
				245					250					255	
Val	Ala	Leu	Leu	Leu	Val	Met	Leu	Leu	Ile	Ile	Val	Cys	His	Lys	Lys
			260					265					270		
Pro	Asn	Gln	Pro	Ser	Arg	Pro	Ser	Asn	Thr	Ala	Ser	Lys	Leu	Glu	Arg
		275					280					285			
Asp	Ser	Asn	Ala	Asp	Arg	Glu	Thr	Ile	Asn	Leu	Lys	Glu	Leu	Glu	Pro
	290					295					300				
Gln	Ile	Ala	Ser	Ala	Lys	Pro	Asn	Ala	Glu						
305					310										

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 223 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 194..223

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

AGNCCCNAGA TTATTTCTCC CTGTATAAGG GACGCCAGG AGGCCTGGGG AGCGGACAAG	60
GCTCCTTTTA CTTTCTTCT TCTTCTATTT TTTTACCTT CTATTTTTTT CTTCATGTTC	120
CTGTGATCTT CGGGAATGCT GCTGTGCTTG TGTGTGTGGT CCCTGAGCGC CGAGGTGGAG	180
AGGCACTGGT GAC ATG TAT GTC ATC AAG ACA TGT GCA ACC TGC	223
Met Tyr Val Ile Lys Thr Cys Ala Thr Cys	
1 5 10	

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 10 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Met Tyr Val Ile Lys Thr Cys Ala Thr Cys
1 5 10

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(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1716 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 249..1166

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

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GAGTTTTATA CCTCAATAGA CTCTTACTAG TTTCTCTTTT TCAGGTTGTG AAACCTCAACC      60
TTCAAAGACA CTCTGTTCCA TTTCTGTGGA CTAATAGGAT CATCTTTAGC ATCTGCCGGG      120
TGGATGCCAT CCAGGCTTCT TTTTCTACAT CTCTGTTTCT CGATTTTGTG GAGCCTAGGA      180

GGTGCCTAAG CTCCATTGGC TCTAGATTCC TGGCTTTCCC CATCATGTTC TCCAAAGCAT      240
CTGAAGCT ATG GCT TGC AAT TGT CAG TTG ATG CAG GAT ACA CCA CTC CTC      290
      Met Ala Cys Asn Cys Gln Leu Met Gln Asp Thr Pro Leu Leu
              1              5              10

AAG TTT CCA TGT CCA AGG CTC AAT CTT CTC TTT GTG CTG CTG ATT CGT      338
Lys Phe Pro Cys Pro Arg Leu Asn Leu Leu Phe Val Leu Leu Ile Arg
      15              20              25              30

CTT TCA CAA GTG TCT TCA GAT GTT GAT GAA CAA CTG TCC AAG TCA GTG      386
Leu Ser Gln Val Ser Ser Asp Val Asp Glu Gln Leu Ser Lys Ser Val
              35              40              45

AAA GAT AAG GTA TTG CTG CCT TGC CGT TAC AAC TCT CCT CAT GAA GAT      434
Lys Asp Lys Val Leu Leu Pro Cys Arg Tyr Asn Ser Pro His Glu Asp
              50              55              60

GAG TCT GAA GAC CGA ATC TAC TGG CAA AAA CAT GAC AAA GTG GTG CTG      482
Glu Ser Glu Asp Arg Ile Tyr Trp Gln Lys His Asp Lys Val Val Leu
              65              70              75

TCT GTC ATT GCT GGG AAA CTA AAA GTG TGG CCC GAG TAT AAG AAC CGG      530
Ser Val Ile Ala Gly Lys Leu Lys Val Trp Pro Glu Tyr Lys Asn Arg
              80              85              90

ACT TTA TAT GAC AAC ACT ACC TAC TCT CTT ATC ATC CTG GGC CTG GTC      578
Thr Leu Tyr Asp Asn Thr Thr Tyr Ser Leu Ile Ile Leu Gly Leu Val
              95              100              105              110

CTT TCA GAC CGG GGC ACA TAC AGC TGT GTC GTT CAA AAG AAG GAA AGA      626
Leu Ser Asp Arg Gly Thr Tyr Ser Cys Val Val Gln Lys Lys Glu Arg
              115              120              125

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GGA ACG TAT GAA GTT AAA CAC TTG GCT TTA GTA AAG TTG TCC ATC AAA	674
Gly Thr Tyr Glu Val Lys His Leu Ala Leu Val Lys Leu Ser Ile Lys	
130 135 140	
GCT GAC TTC TCT ACC CCC AAC ATA ACT GAG TCT GGA AAC CCA TCT GCA	722
Ala Asp Phe Ser Thr Pro Asn Ile Thr Glu Ser Gly Asn Pro Ser Ala	
145 150 155	
GAC ACT AAA AGG ATT ACC TGC TTT GCT TCC GGG GGT TTC CCA AAG CCT	770
Asp Thr Lys Arg Ile Thr Cys Phe Ala Ser Gly Gly Phe Pro Lys Pro	
160 165 170	
CGC TTC TCT TGG TTG GAA AAT GGA AGA GAA TTA CCT GGC ATC AAT ACG	818
Arg Phe Ser Trp Leu Glu Asn Gly Arg Glu Leu Pro Gly Ile Asn Thr	
175 180 185 190	
ACA ATT TCC CAG GAT CCT GAA TCT GAA TTG TAC ACC ATT AGT AGC CAA	866
Thr Ile Ser Gln Asp Pro Glu Ser Glu Leu Tyr Thr Ile Ser Ser Gln	
195 200 205	
CTA GAT TTC AAT ACG ACT CGC AAC CAC ACC ATT AAG TGT CTC ATT AAA	914
Leu Asp Phe Asn Thr Thr Arg Asn His Thr Ile Lys Cys Leu Ile Lys	
210 215 220	
TAT GGA GAT GCT CAC GTG TCA GAG GAC TTC ACC TGG GAA AAA CCC CCA	962
Tyr Gly Asp Ala His Val Ser Glu Asp Phe Thr Trp Glu Lys Pro Pro	
225 230 235	
GAA GAC CCT CCT GAT AGC AAG AAC ACA CTT GTG CTC TTT GGG GCA GGA	1010
Glu Asp Pro Pro Asp Ser Lys Asn Thr Leu Val Leu Phe Gly Ala Gly	
240 245 250	
TTC GGC GCA GTA ATA ACA GTC GTC GTC ATC GTT GTC ATC ATC AAA TGC	1058
Phe Gly Ala Val Ile Thr Val Val Val Ile Val Val Ile Ile Lys Cys	
255 260 265 270	
TTC TGT AAG CAC AGA AGC TGT TTC AGA AGA AAT GAG GCA AGC AGA GAA	1106
Phe Cys Lys His Arg Ser Cys Phe Arg Arg Asn Glu Ala Ser Arg Glu	
275 280 285	
ACA AAC AAC AGC CTT ACC TTC GGG CCT GAA GAA GCA TTA GCT GAA CAG	1154
Thr Asn Asn Ser Leu Thr Phe Gly Pro Glu Glu Ala Leu Ala Glu Gln	
290 295 300	
ACC GTC TTC CTT TAGTTCTTCT CTGTCCATGT GGGATACATG GTATTATGTG	1206
Thr Val Phe Leu	
305	
GCTCATGAGG TACAATCTTT CTTTCAGCAC CGTGCTAGCT GATCTTTCGG ACAACTTGAC	1266
ACAAGATAGA GTTAACTGGG AAGAGAAAGC CTTGAATGAG GATTTCTTTC CATCAGGAAG	1326
CTACGGGCAA GTTTGCTGGG CCTTTGATTG CTTGATGACT GAAGTGGAAA GGCTGAGCCC	1386
ACTGTGGGTG GTGCTAGCCC TGGGCAGGGG CAGGTGACCC TGGGTGGTAT AAGAAAAAGA	1446
GCTGTCACTA AAAGGAGAGG TGCCTAGTCT TACTGCAACT TGATATGTCA TGTTTGGTTG	1506

GTGTCTGTGG GAGGCCTGCC CTTTCTGAA GAGAAGTGGT GGGAGAGTGG ATGGGGTGGG 1566
 GGCAGAGGAA AAGTGGGGGA GAGGGCCTGG GAGGAGAGGA GGGAGGGGGA CGGGGTGGGG 1626
 GTGGGGAAAA CTATGGTTGG GATGTAAAAA CGGATAATAA TATAAATATT AAATAAAAAG 1686
 AGAGTATTGA GCAAAAAAAA AAAAAAAAAA 1716

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 306 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Met	Ala	Cys	Asn	Cys	Gln	Leu	Met	Gln	Asp	Thr	Pro	Leu	Leu	Lys	Phe	1	5	10	15
Pro	Cys	Pro	Arg	Leu	Ile	Leu	Leu	Phe	Val	Leu	Leu	Ile	Arg	Leu	Ser	20	25	30	
Gln	Val	Ser	Ser	Asp	Val	Asp	Glu	Gln	Leu	Ser	Lys	Ser	Val	Lys	Asp	35	40	45	
Lys	Val	Leu	Leu	Pro	Cys	Arg	Tyr	Asn	Ser	Pro	His	Glu	Asp	Glu	Ser	50	55	60	
Glu	Asp	Arg	Ile	Tyr	Trp	Gln	Lys	His	Asp	Lys	Val	Val	Leu	Ser	Val	65	70	75	80
Ile	Ala	Gly	Lys	Leu	Lys	Val	Trp	Pro	Glu	Tyr	Lys	Asn	Arg	Thr	Leu	85	90	95	
Tyr	Asp	Asn	Thr	Thr	Tyr	Ser	Leu	Ile	Ile	Leu	Gly	Leu	Val	Leu	Ser	100	105	110	
Asp	Arg	Gly	Thr	Tyr	Ser	Cys	Val	Val	Gln	Lys	Lys	Glu	Arg	Gly	Thr	115	120	125	
Tyr	Glu	Val	Lys	His	Leu	Ala	Leu	Val	Lys	Leu	Ser	Ile	Lys	Ala	Asp	130	135	140	
Phe	Ser	Thr	Pro	Asn	Ile	Thr	Glu	Ser	Gly	Asn	Pro	Ser	Ala	Asp	Thr	145	150	155	160
Lys	Arg	Ile	Thr	Cys	Phe	Ala	Ser	Gly	Gly	Phe	Pro	Lys	Pro	Arg	Phe	165	170	175	
Ser	Trp	Leu	Glu	Asn	Gly	Arg	Glu	Leu	Pro	Gly	Ile	Asn	Thr	Thr	Ile	180	185	190	
Ser	Gln	Asp	Pro	Glu	Ser	Glu	Leu	Tyr	Thr	Ile	Ser	Ser	Gln	Leu	Asp	195	200	205	

Phe Asn Thr Thr Arg Asn His Thr Ile Lys Cys Leu Ile Lys Tyr Gly
 210 215 220
 Asp Ala His Val Ser Glu Asp Phe Thr Trp Glu Lys Pro Pro Glu Asp
 225 230 235 240
 Pro Pro Asp Ser Lys Asn Thr Leu Val Leu Phe Gly Ala Gly Phe Gly
 245 250 255
 Ala Val Ile Thr Val Val Val Ile Val Val Ile Ile Lys Cys Phe Cys
 260 265 270
 Lys His Arg Ser Cys Phe Arg Arg Asn Glu Ala Ser Arg Glu Thr Asn
 275 280 285
 Asn Ser Leu Thr Phe Gly Pro Glu Glu Ala Leu Ala Glu Gln Thr Val
 290 295 300
 Phe Leu
 305

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1491 base pairs
 (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
 (B) LOCATION: 318..1181

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CCAAAGAAAA AGTGATTGTG CATTGCTTTA TAGACTGTAA GAAGAGAACA TCTCAGAAGT 60
 GGAGTCTTAC CCTGAAATCA AAGGATTTAA AGAAAAAGTG GAATTTTCTC TCAGCAAGCT 120
 GTGAAACTAA ATCCACAACC TTTGGAGACC CAGGAACACC CTCCAATCTC TGTGTGTTTT 180
 GTAAACATCA CTGGAGGGTC TTCTACGTGA GCAATTGGAT TGTCATCAGC CCTGCCTGTT 240
 TTGCACCTGG GAAGTGCCCT GGTCTTACTT GGGTCCAAAT TGTTGGCTTT CACTTTTGAC 300
 CCTAAGCATC TGAAGCC ATG GGC CAC ACA CGG AGG CAG GGA ACA TCA CCA 350
 Met Gly His Thr Arg Arg Gln Gly Thr Ser Pro
 1 5 10
 TCC AAG TGT CCA TAC CTG AAT TTC TTT CAG CTC TTG GTG CTG GCT GGT 398
 Ser Lys Cys Pro Tyr Leu Asn Phe Phe Gln Leu Leu Val Leu Ala Gly
 15 20 25

CTT	TCT	CAC	TTC	TGT	TCA	GGT	GTT	ATC	CAC	GTG	ACC	AAG	GAA	GTG	AAA	446
Leu	Ser	His	Phe	Cys	Ser	Gly	Val	Ile	His	Val	Thr	Lys	Glu	Val	Lys	
		30					35					40				
GAA	GTG	GCA	ACG	CTG	TCC	TGT	GGT	CAC	AAT	GTT	TCT	GTT	GAA	GAG	CTG	494
Glu	Val	Ala	Thr	Leu	Ser	Cys	Gly	His	Asn	Val	Ser	Val	Glu	Glu	Leu	
	45					50				55						
GCA	CAA	ACT	CGC	ATC	TAC	TGG	CAA	AAG	GAG	AAG	AAA	ATG	GTG	CTG	ACT	542
Ala	Gln	Thr	Arg	Ile	Tyr	Trp	Gln	Lys	Glu	Lys	Lys	Met	Val	Leu	Thr	
	60				65					70					75	
ATG	ATG	TCT	GGG	GAC	ATG	AAT	ATA	TGG	CCC	GAG	TAC	AAG	AAC	CGG	ACC	590
Met	Met	Ser	Gly	Asp	Met	Asn	Ile	Trp	Pro	Glu	Tyr	Lys	Asn	Arg	Thr	
				80					85					90		
ATC	TTT	GAT	ATC	ACT	AAT	AAC	CTC	TCC	ATT	GTG	ATC	CTG	GCT	CTG	CGC	638
Ile	Phe	Asp	Ile	Thr	Asn	Asn	Leu	Ser	Ile	Val	Ile	Leu	Ala	Leu	Arg	
			95					100						105		
CCA	TCT	GAC	GAG	GGC	ACA	TAC	GAG	TGT	GTT	GTT	CTG	AAG	TAT	GAA	AAA	686
Pro	Ser	Asp	Glu	Gly	Thr	Tyr	Glu	Cys	Val	Val	Leu	Lys	Tyr	Glu	Lys	
		110					115					120				
GAC	GCT	TTC	AAG	CGG	GAA	CAC	CTG	GCT	GAA	GTG	ACG	TTA	TCA	GTC	AAA	734
Asp	Ala	Phe	Lys	Arg	Glu	His	Leu	Ala	Glu	Val	Thr	Leu	Ser	Val	Lys	
	125					130					135					
GCT	GAC	TTC	CCT	ACA	CCT	AGT	ATA	TCT	GAC	TTT	GAA	ATT	CCA	ACT	TCT	782
Ala	Asp	Phe	Pro	Thr	Pro	Ser	Ile	Ser	Asp	Phe	Glu	Ile	Pro	Thr	Ser	
	140					145				150					155	
AAT	ATT	AGA	AGG	ATA	ATT	TGC	TCA	ACC	TCT	GGA	GGT	TTT	CCA	GAG	CCT	830
Asn	Ile	Arg	Arg	Ile	Ile	Cys	Ser	Thr	Ser	Gly	Gly	Phe	Pro	Glu	Pro	
				160					165					170		
CAC	CTC	TCC	TGG	TTG	GAA	AAT	GGA	GAA	GAA	TTA	AAT	GCC	ATC	AAC	ACA	878
His	Leu	Ser	Trp	Leu	Glu	Asn	Gly	Glu	Glu	Leu	Asn	Ala	Ile	Asn	Thr	
			175					180					185			
ACA	GTT	TCC	CAA	GAT	CCT	GAA	ACT	GAG	CTC	TAT	GCT	GTT	AGC	AGC	AAA	926
Thr	Val	Ser	Gln	Asp	Pro	Glu	Thr	Glu	Leu	Tyr	Ala	Val	Ser	Ser	Lys	
		190					195					200				
CTG	GAT	TTC	AAT	ATG	ACA	ACC	AAC	CAC	AGC	TTC	ATG	TGT	CTC	ATC	AAG	974
Leu	Asp	Phe	Asn	Met	Thr	Thr	Asn	His	Ser	Phe	Met	Cys	Leu	Ile	Lys	
	205					210					215					
TAT	GGA	CAT	TTA	AGA	GTG	AAT	CAG	ACC	TTC	AAC	TGG	AAT	ACA	ACC	AAG	1022
Tyr	Gly	His	Leu	Arg	Val	Asn	Gln	Thr	Phe	Asn	Trp	Asn	Thr	Thr	Lys	
	220				225					230					235	
CAA	GAG	CAT	TTT	CCT	GAT	AAC	CTG	CTC	CCA	TCC	TGG	GCC	ATT	ACC	TTA	1070
Gln	Glu	His	Phe	Pro	Asp	Asn	Leu	Leu	Pro	Ser	Trp	Ala	Ile	Thr	Leu	
				240					245					250		
ATC	TCA	GTA	AAT	GGA	ATT	TTT	GTG	ATA	TGC	TGC	CTG	ACC	TAC	TGC	TTT	1118

Ile Ser Val Asn Gly Ile Phe Val Ile Cys Cys Leu Thr Tyr Cys Phe	
255 260 265	
GCC CCA AGA TGC AGA GAG AGA AGG AGG AAT GAG AGA TTG AGA AGG GAA	1166
Ala Pro Arg Cys Arg Glu Arg Arg Arg Asn Glu Arg Leu Arg Arg Glu	
270 275 280	
AGT GTA CGC CCT GTA TAACAGTGTC CGCAGAAGCA AGGGGCTGAA AAGATCTGAA	1221
Ser Val Arg Pro Val	
285	
GGTAGCCTCC GTCATCTCTT CTGGGATACA TGGATCGTGG GGATCATGAG GCATTCTTCC	1281
CTTAACAAAT TTAAGCTGTT TTACCCACTA CCTCACCTTC TTAAAAACCT CTTTCAGATT	1341
AAGCTGAACA GTTACAAGAT GGCTGGCATC CCTCTCCTTT CTCCCCATAT GCAATTTGCT	1401
TAATGTAACC TCTTCTTTTG CCATGTTTCC ATTCTGCCAT CTTGAATTGT CTTGTCAGCC	1461
AATTCATTAT CTATTAAACA CTAATTTGAG	1491

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 288 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Met Gly His Thr Arg Arg Gln Gly Thr Ser Pro Ser Lys Cys Pro Tyr	
1 5 10 15	
Leu Asn Phe Phe Gln Leu Leu Val Leu Ala Gly Leu Ser His Phe Cys	
20 25 30	
Ser Gly Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu	
35 40 45	
Ser Cys Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile	
50 55 60	
Tyr Trp Gln Lys Glu Lys Lys Met Val Leu Thr Met Met Ser Gly Asp	
65 70 75 80	
Met Asn Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr	
85 90 95	
Asn Asn Leu Ser Ile Val Ile Leu Ala Leu Arg Pro Ser Asp Glu Gly	
100 105 110	
Thr Tyr Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg	
115 120 125	
Glu His Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp Phe Pro Thr	

130	135	140
Pro Ser Ile Ser Asp Phe Glu Ile Pro Thr Ser Asn Ile Arg Arg Ile		
145	150	155 160
Ile Cys Ser Thr Ser Gly Gly Phe Pro Glu Pro His Leu Ser Trp Leu		
	165	170 175
Glu Asn Gly Glu Glu Leu Asn Ala Ile Asn Thr Thr Val Ser Gln Asp		
	180	185 190
Pro Glu Thr Glu Leu Tyr Ala Val Ser Ser Lys Leu Asp Phe Asn Met		
	195	200 205
Thr Thr Asn His Ser Phe Met Cys Leu Ile Lys Tyr Gly His Leu Arg		
	210	215 220
Val Asn Gln Thr Phe Asn Trp Asn Thr Thr Lys Gln Glu His Phe Pro		
225	230	235 240
Asp Asn Leu Leu Pro Ser Trp Ala Ile Thr Leu Ile Ser Val Asn Gly		
	245	250 255
Ile Phe Val Ile Cys Cys Leu Thr Tyr Cys Phe Ala Pro Arg Cys Arg		
	260	265 270
Glu Arg Arg Arg Asn Glu Arg Leu Arg Arg Glu Ser Val Arg Pro Val		
	275	280 285

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1151 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 99..1025

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

GGAGCAAGCA GACGCGTAAG AGTGGCTCCT GTAGGCAGCA CGGACTTGAA CAACCAGACT	60
CCTGTAGACG TGTTCCAGAA CTTACGGAAG CACCCACG ATG GAC CCC AGA TGC	113
Met Asp Pro Arg Cys	
1 5	
ACC ATG GGC TTG GCA ATC CTT ATC TTT GTG ACA GTC TTG CTG ATC TCA	161
Thr Met Gly Leu Ala Ile Leu Ile Phe Val Thr Val Leu Leu Ile Ser	
10 15 20	

GAT	GCT	GTT	TCC	GTG	GAG	ACG	CAA	GCT	TAT	TTC	AAT	GGG	ACT	GCA	TAT	209
Asp	Ala	Val	Ser	Val	Glu	Thr	Gln	Ala	Tyr	Phe	Asn	Gly	Thr	Ala	Tyr	
			25					30						35		
CTG	CCG	TGC	CCA	TTT	ACA	AAG	GCT	CAA	AAC	ATA	AGC	CTG	AGT	GAG	CTG	257
Leu	Pro	Cys	Pro	Phe	Thr	Lys	Ala	Gln	Asn	Ile	Ser	Leu	Ser	Glu	Leu	
		40					45					50				
GTA	GTA	TTT	TGG	CAG	GAC	CAG	CAA	AAG	TTG	GTT	CTG	TAC	GAG	CAC	TAT	305
Val	Val	Phe	Trp	Gln	Asp	Gln	Gln	Lys	Leu	Val	Leu	Tyr	Glu	His	Tyr	
		55				60					65					
TTG	GGC	ACA	GAG	AAA	CTT	GAT	AGT	GTG	AAT	GCC	AAG	TAC	CTG	GGC	CGC	353
Leu	Gly	Thr	Glu	Lys	Leu	Asp	Ser	Val	Asn	Ala	Lys	Tyr	Leu	Gly	Arg	
70					75				80					85		
ACG	AGC	TTT	GAC	AGG	AAC	AAC	TGG	ACT	CTA	CGA	CTT	CAC	AAT	GTT	CAG	401
Thr	Ser	Phe	Asp	Arg	Asn	Asn	Trp	Thr	Leu	Arg	Leu	His	Asn	Val	Gln	
				90					95					100		
ATC	AAG	GAC	ATG	GGC	TCG	TAT	GAT	TGT	TTT	ATA	CAA	AAA	AAG	CCA	CCC	449
Ile	Lys	Asp	Met	Gly	Ser	Tyr	Asp	Cys	Phe	Ile	Gln	Lys	Lys	Pro	Pro	
			105					110					115			
ACA	GGA	TCA	ATT	ATC	CTC	CAA	CAG	ACA	TTA	ACA	GAA	CTG	TCA	GTG	ATC	497
Thr	Gly	Ser	Ile	Ile	Leu	Gln	Gln	Thr	Leu	Thr	Glu	Leu	Ser	Val	Ile	
			120				125					130				
GCC	AAC	TTC	AGT	GAA	CCT	GAA	ATA	AAA	CTG	GCT	CAG	AAT	GTA	ACA	GGA	545
Ala	Asn	Phe	Ser	Glu	Pro	Glu	Ile	Lys	Leu	Ala	Gln	Asn	Val	Thr	Gly	
		135				140					145					
AAT	TCT	GGC	ATA	AAT	TTG	ACC	TGC	ACG	TCT	AAG	CAA	GGT	CAC	CCG	AAA	593
Asn	Ser	Gly	Ile	Asn	Leu	Thr	Cys	Thr	Ser	Lys	Gln	Gly	His	Pro	Lys	
150					155					160					165	
CCT	AAG	AAG	ATG	TAT	TTT	CTG	ATA	ACT	AAT	TCA	ACT	AAT	GAG	TAT	GGT	641
Pro	Lys	Lys	Met	Tyr	Phe	Leu	Ile	Thr	Asn	Ser	Thr	Asn	Glu	Tyr	Gly	
				170					175					180		
GAT	AAC	ATG	CAG	ATA	TCA	CAA	GAT	AAT	GTC	ACA	GAA	CTG	TTC	AGT	ATC	689
Asp	Asn	Met	Gln	Ile	Ser	Gln	Asp	Asn	Val	Thr	Glu	Leu	Phe	Ser	Ile	
			185					190					195			
TCC	AAC	AGC	CTC	TCT	CTT	TCA	TTC	CCG	GAT	GGT	GTG	TGG	CAT	ATG	ACC	737
Ser	Asn	Ser	Leu	Ser	Leu	Ser	Phe	Pro	Asp	Gly	Val	Trp	His	Met	Thr	
		200					205					210				
GTT	GTG	TGT	GTT	CTG	GAA	ACG	GAG	TCA	ATG	AAG	ATT	TCC	TCC	AAA	CCT	785
Val	Val	Cys	Val	Leu	Glu	Thr	Glu	Ser	Met	Lys	Ile	Ser	Ser	Lys	Pro	
		215				220					225					
CTC	AAT	TTC	ACT	CAA	GAG	TTT	CCA	TCT	CCT	CAA	ACG	TAT	TGG	AAG	GAG	833
Leu	Asn	Phe	Thr	Gln	Glu	Phe	Pro	Ser	Pro	Gln	Thr	Tyr	Trp	Lys	Glu	
230					235					240					245	
ATT	ACA	GCT	TCA	GTT	ACT	GTG	GCC	CTC	CTC	CTT	GTG	ATG	CTG	CTC	ATC	881
Ile	Thr	Ala	Ser	Val	Thr	Val	Ala	Leu	Leu	Leu	Val	Met	Leu	Leu	Ile	
				250					255					260		

ATT GTA TGT CAC AAG AAG CCG AAT CAG CCT AGC AGG CCC AGC AAC ACA 929
 Ile Val Cys His Lys Lys Pro Asn Gln Pro Ser Arg Pro Ser Asn Thr
 265 270 275
 GCC TCT AAG TTA GAG CGG GAT AGT AAC GCT GAC AGA GAG ACT ATC AAC 977
 Ala Ser Lys Leu Glu Arg Asp Ser Asn Ala Asp Arg Glu Thr Ile Asn
 280 285 290
 CTG AAG GAA CTT GAA CCC CAA ATT GCT TCA GCA AAA CCA AAT GCA GAG 1025
 Leu Lys Glu Leu Glu Pro Gln Ile Ala Ser Ala Lys Pro Asn Ala Glu
 295 300 305
 TGAAGGCAGT GAGAGCCTGA GGAAAGAGTT AAAAATTGCT TTGCCTGAAA TAAGAAGTGC 1085
 AGAGTTTCTC AGAATTCAAA AATGTTCTCA GCTGATTGGA ATTCTACAGT TGAATAATTA 1145
 AAGAAC 1151

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 309 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Met Asp Pro Arg Cys Thr Met Gly Leu Ala Ile Leu Ile Phe Val Thr
 1 5 10 15
 Val Leu Leu Ile Ser Asp Ala Val Ser Val Glu Thr Gln Ala Tyr Phe
 20 25 30
 Asn Gly Thr Ala Tyr Leu Pro Cys Pro Phe Thr Lys Ala Gln Asn Ile
 35 40 45
 Ser Leu Ser Glu Leu Val Val Phe Trp Gln Asp Gln Gln Lys Leu Val
 50 55 60
 Leu Tyr Glu His Tyr Leu Gly Thr Glu Lys Leu Asp Ser Val Asn Ala
 65 70 75 80
 Lys Tyr Leu Gly Arg Thr Ser Phe Asp Arg Asn Asn Trp Thr Leu Arg
 85 90 95
 Leu His Asn Val Gln Ile Lys Asp Met Gly Ser Tyr Asp Cys Phe Ile
 100 105 110
 Gln Lys Lys Pro Pro Thr Gly Ser Ile Ile Leu Gln Gln Thr Leu Thr
 115 120 125
 Glu Leu Ser Val Ile Ala Asn Phe Ser Glu Pro Glu Ile Lys Leu Ala
 130 135 140

Gln Asn Val Thr Gly Asn Ser Gly Ile Asn Leu Thr Cys Thr Ser Lys
145 150 155 160

Gln Gly His Pro Lys Pro Lys Lys Met Tyr Phe Leu Ile Thr Asn Ser
165 170 175

Thr Asn Glu Tyr Gly Asp Asn Met Gln Ile Ser Gln Asp Asn Val Thr
180 185 190

Glu Leu Phe Ser Ile Ser Asn Ser Leu Ser Leu Ser Phe Pro Asp Gly
195 200 205

Val Trp His Met Thr Val Val Cys Val Leu Glu Thr Glu Ser Met Lys
210 215 220

Ile Ser Ser Lys Pro Leu Asn Phe Thr Gln Glu Phe Pro Ser Pro Gln
225 230 235 240

Thr Tyr Trp Lys Glu Ile Thr Ala Ser Val Thr Val Ala Leu Leu Leu
245 250 255

Val Met Leu Leu Ile Ile Val Cys His Lys Lys Pro Asn Gln Pro Ser
260 265 270

Arg Pro Ser Asn Thr Ala Ser Lys Leu Glu Arg Asp Ser Asn Ala Asp
275 280 285

Arg Glu Thr Ile Asn Leu Lys Glu Leu Glu Pro Gln Ile Ala Ser Ala
290 295 300

Lys Pro Asn Ala Glu
305

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1120 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 107..1093

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

CACAGGGTGA AAGCTTTGCT TCTCTGCTGC TGTAACAGGG ACTAGCACAG ACACACGGAT 60

GAGTGGGGTC ATTTCCAGAT ATTAGGTCAC AGCAGAAGCA GCCAAA ATG GAT CCC 115
Met Asp Pro
1

CAG TGC ACT ATG GGA CTG AGT AAC ATT CTC TTT GTG ATG GCC TTC CTG 163
Gln Cys Thr Met Gly Leu Ser Asn Ile Leu Phe Val Met Ala Phe Leu

5	10	15	
CTC TCT GGT GCT GCT CCT CTG AAG ATT CAA GCT TAT TTC AAT GAG ACT			211
Leu Ser Gly Ala Ala Pro Leu Lys Ile Gln Ala Tyr Phe Asn Glu Thr			
20	25	30	35
GCA GAC CTG CCA TGC CAA TTT GCA AAC TCT CAA AAC CAA AGC CTG AGT			259
Ala Asp Leu Pro Cys Gln Phe Ala Asn Ser Gln Asn Gln Ser Leu Ser			
	40	45	50
GAG CTA GTA GTA TTT TGG CAG GAC CAG GAA AAC TTG GTT CTG AAT GAG			307
Glu Leu Val Val Phe Trp Gln Asp Gln Glu Asn Leu Val Leu Asn Glu			
	55	60	65
GTA TAC TTA GGC AAA GAG AAA TTT GAC AGT GTT CAT TCC AAG TAT ATG			355
Val Tyr Leu Gly Lys Glu Lys Phe Asp Ser Val His Ser Lys Tyr Met			
	70	75	80
GGC CGC ACA AGT TTT GAT TCG GAC AGT TGG ACC CTG AGA CTT CAC AAT			403
Gly Arg Thr Ser Phe Asp Ser Asp Ser Trp Thr Leu Arg Leu His Asn			
	85	90	95
CTT CAG ATC AAG GAC AAG GGC TTG TAT CAA TGT ATC ATC CAT CAC AAA			451
Leu Gln Ile Lys Asp Lys Gly Leu Tyr Gln Cys Ile Ile His His Lys			
100	105	110	115
AAG CCC ACA GGA ATG ATT CGC ATC CAC CAG ATG AAT TCT GAA CTG TCA			499
Lys Pro Thr Gly Met Ile Arg Ile His Gln Met Asn Ser Glu Leu Ser			
	120	125	130
GTG CTT GCT AAC TTC AGT CAA CCT GAA ATA GTA CCA ATT TCT AAT ATA			547
Val Leu Ala Asn Phe Ser Gln Pro Glu Ile Val Pro Ile Ser Asn Ile			
	135	140	145
ACA GAA AAT GTG TAC ATA AAT TTG ACC TGC TCA TCT ATA CAC GGT TAC			595
Thr Glu Asn Val Tyr Ile Asn Leu Thr Cys Ser Ser Ile His Gly Tyr			
	150	155	160
CCA GAA CCT AAG AAG ATG AGT GTT TTG CTA AGA ACC AAG AAT TCA ACT			643
Pro Glu Pro Lys Lys Met Ser Val Leu Leu Arg Thr Lys Asn Ser Thr			
165	170	175	
ATC GAG TAT GAT GGT ATT ATG CAG AAA TCT CAA GAT AAT GTC ACA GAA			691
Ile Glu Tyr Asp Gly Ile Met Gln Lys Ser Gln Asp Asn Val Thr Glu			
180	185	190	195
CTG TAC GAC GTT TCC ATC AGC TTG TCT GTT TCA TTC CCT GAT GTT ACG			739
Leu Tyr Asp Val Ser Ile Ser Leu Ser Val Ser Phe Pro Asp Val Thr			
	200	205	210
AGC AAT ATG ACC ATC TTC TGT ATT CTG GAA ACT GAC AAG ACG CGG CTT			787
Ser Asn Met Thr Ile Phe Cys Ile Leu Glu Thr Asp Lys Thr Arg Leu			
	215	220	225
TTA TCT TCA CCT TTC TCT ATA GAG CTT GAG GAC CCT CAG CCT CCC CCA			835
Leu Ser Ser Pro Phe Ser Ile Glu Leu Glu Asp Pro Gln Pro Pro Pro			
	230	235	240

GAC CAC ATT CCT TGG ATT ACA GCT GTA CTT CCA ACA GTT ATT ATA TGT	883
Asp His Ile Pro Trp Ile Thr Ala Val Leu Pro Thr Val Ile Ile Cys	
245 250 255	
GTG ATG GTT TTC TGT CTA ATT CTA TGG AAA TGG AAG AAG AAG AAG CGG	931
Val Met Val Phe Cys Leu Ile Leu Trp Lys Trp Lys Lys Lys Lys Arg	
260 265 270 275	
CCT CGC AAC TCT TAT AAA TGT GGA ACC AAC ACA ATG GAG AGG GAA GAG	979
Pro Arg Asn Ser Tyr Lys Cys Gly Thr Asn Thr Met Glu Arg Glu Glu	
280 285 290	
AGT GAA CAG ACC AAG AAA AGA GAA AAA ATC CAT ATA CCT GAA AGA TCT	1027
Ser Glu Gln Thr Lys Lys Arg Glu Lys Ile His Ile Pro Glu Arg Ser	
295 300 305	
GAT GAA GCC CAG CGT GTT TTT AAA AGT TCG AAG ACA TCT TCA TGC GAC	1075
Asp Glu Ala Gln Arg Val Phe Lys Ser Ser Lys Thr Ser Ser Cys Asp	
310 315 320	
AAA AGT GAT ACA TGT TTT TAATTAAAGA GTAAAGCCCA AAAAAAA	1120
Lys Ser Asp Thr Cys Phe	
325	

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 329 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Met Asp Pro Gln Cys Thr Met Gly Leu Ser Asn Ile Leu Phe Val Met	
1 5 10 15	
Ala Phe Leu Leu Ser Gly Ala Ala Pro Leu Lys Ile Gln Ala Tyr Phe	
20 25 30	
Asn Glu Thr Ala Asp Leu Pro Cys Gln Phe Ala Asn Ser Gln Asn Gln	
35 40 45	
Ser Leu Ser Glu Leu Val Val Phe Trp Gln Asp Gln Glu Asn Leu Val	
50 55 60	
Leu Asn Glu Val Tyr Leu Gly Lys Glu Lys Phe Asp Ser Val His Ser	
65 70 75 80	
Lys Tyr Met Gly Arg Thr Ser Phe Asp Ser Asp Ser Trp Thr Leu Arg	
85 90 95	
Leu His Asn Leu Gln Ile Lys Asp Lys Gly Leu Tyr Gln Cys Ile Ile	
100 105 110	
His His Lys Lys Pro Thr Gly Met Ile Arg Ile His Gln Met Asn Ser	

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115	120	125
Glu Leu Ser Val Leu Ala Asn Phe Ser Gln Pro Glu Ile Val Pro Ile		
130	135	140
Ser Asn Ile Thr Glu Asn Val Tyr Ile Asn Leu Thr Cys Ser Ser Ile		
145	150	155
His Gly Tyr Pro Glu Pro Lys Lys Met Ser Val Leu Leu Arg Thr Lys		
	165	170
Asn Ser Thr Ile Glu Tyr Asp Gly Ile Met Gln Lys Ser Gln Asp Asn		
	180	190
Val Thr Glu Leu Tyr Asp Val Ser Ile Ser Leu Ser Val Ser Phe Pro		
	195	205
Asp Val Thr Ser Asn Met Thr Ile Phe Cys Ile Leu Glu Thr Asp Lys		
	210	220
Thr Arg Leu Leu Ser Ser Pro Phe Ser Ile Glu Leu Glu Asp Pro Gln		
	225	235
Pro Pro Pro Asp His Ile Pro Trp Ile Thr Ala Val Leu Pro Thr Val		
	245	250
Ile Ile Cys Val Met Val Phe Cys Leu Ile Leu Trp Lys Trp Lys Lys		
	260	270
Lys Lys Arg Pro Arg Asn Ser Tyr Lys Cys Gly Thr Asn Thr Met Glu		
	275	285
Arg Glu Glu Ser Glu Gln Thr Lys Lys Arg Glu Lys Ile His Ile Pro		
	290	300
Glu Arg Ser Asp Glu Ala Gln Arg Val Phe Lys Ser Ser Lys Thr Ser		
	305	315
Ser Cys Asp Lys Ser Asp Thr Cys Phe		
	325	

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1161 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 148..1134

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

AGGAGCCTTA GGAGGTACGG GGAGCTCGCA AATACTCCTT TTGGTTTATT CTTACCACCT	60
TGCTTCTGTG TTCCTTGGGA ATGCTGCTGT GCTTATGCAT CTGGTCTCTT TTTGGAGCTA	120
CAGTGGACAG GCATTTGTGA CAGCACT ATG GAT CCC CAG TGC ACT ATG GGA	171
Met Asp Pro Gln Cys Thr Met Gly	
1 5	
CTG AGT AAC ATT CTC TTT GTG ATG GCC TTC CTG CTC TCT GGT GCT GCT	219
Leu Ser Asn Ile Leu Phe Val Met Ala Phe Leu Leu Ser Gly Ala Ala	
10 15 20	
CCT CTG AAG ATT CAA GCT TAT TTC AAT GAG ACT GCA GAC CTG CCA TGC	267
Pro Leu Lys Ile Gln Ala Tyr Phe Asn Glu Thr Ala Asp Leu Pro Cys	
25 30 35 40	
CAA TTT GCA AAC TCT CAA AAC CAA AGC CTG AGT GAG CTA GTA GTA TTT	315
Gln Phe Ala Asn Ser Gln Asn Gln Ser Leu Ser Glu Leu Val Val Phe	
45 50 55	
TGG CAG GAC CAG GAA AAC TTG GTT CTG AAT GAG GTA TAC TTA GGC AAA	363
Trp Gln Asp Gln Glu Asn Leu Val Leu Asn Glu Val Tyr Leu Gly Lys	
60 65 70	
GAG AAA TTT GAC AGT GTT CAT TCC AAG TAT ATG GGC CGC ACA AGT TTT	411
Glu Lys Phe Asp Ser Val His Ser Lys Tyr Met Gly Arg Thr Ser Phe	
75 80 85	
GAT TCG GAC AGT TGG ACC CTG AGA CTT CAC AAT CTT CAG ATC AAG GAC	459
Asp Ser Asp Ser Trp Thr Leu Arg Leu His Asn Leu Gln Ile Lys Asp	
90 95 100	
AAG GGC TTG TAT CAA TGT ATC ATC CAT CAC AAA AAG CCC ACA GGA ATG	507
Lys Gly Leu Tyr Gln Cys Ile Ile His His Lys Lys Pro Thr Gly Met	
105 110 115 120	
ATT CGC ATC CAC CAG ATG AAT TCT GAA CTG TCA GTG CTT GCT AAC TTC	555
Ile Arg Ile His Gln Met Asn Ser Glu Leu Ser Val Leu Ala Asn Phe	
125 130 135	
AGT CAA CCT GAA ATA GTA CCA ATT TCT AAT ATA ACA GAA AAT GTG TAC	603
Ser Gln Pro Glu Ile Val Pro Ile Ser Asn Ile Thr Glu Asn Val Tyr	
140 145 150	
ATA AAT TTG ACC TGC TCA TCT ATA CAC GGT TAC CCA GAA CCT AAG AAG	651
Ile Asn Leu Thr Cys Ser Ser Ile His Gly Tyr Pro Glu Pro Lys Lys	
155 160 165	
ATG AGT GTT TTG CTA AGA ACC AAG AAT TCA ACT ATC GAG TAT GAT GGT	699
Met Ser Val Leu Leu Arg Thr Lys Asn Ser Thr Ile Glu Tyr Asp Gly	
170 175 180	
ATT ATG CAG AAA TCT CAA GAT AAT GTC ACA GAA CTG TAC GAC GTT TCC	747
Ile Met Gln Lys Ser Gln Asp Asn Val Thr Glu Leu Tyr Asp Val Ser	
185 190 195 200	
ATC AGC TTG TCT GTT TCA TTC CCT GAT GTT ACG AGC AAT ATG ACC ATC	795

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Ile	Ser	Leu	Ser	Val	Ser	Phe	Pro	Asp	Val	Thr	Ser	Asn	Met	Thr	Ile		
				205					210					215			
TTC	TGT	ATT	CTG	GAA	ACT	GAC	AAG	ACG	CGG	CTT	TTA	TCT	TCA	CCT	TTC	843	
Phe	Cys	Ile	Leu	Glu	Thr	Asp	Lys	Thr	Arg	Leu	Leu	Ser	Ser	Pro	Phe		
			220					225					230				
TCT	ATA	GAG	CTT	GAG	GAC	CCT	CAG	CCT	CCC	CCA	GAC	CAC	ATT	CCT	TGG	891	
Ser	Ile	Glu	Leu	Glu	Asp	Pro	Gln	Pro	Pro	Pro	Asp	His	Ile	Pro	Trp		
		235					240					245					
ATT	ACA	GCT	GTA	CTT	CCA	ACA	GTT	ATT	ATA	TGT	GTG	ATG	GTT	TTC	TGT	939	
Ile	Thr	Ala	Val	Leu	Pro	Thr	Val	Ile	Ile	Cys	Val	Met	Val	Phe	Cys		
	250					255					260						
CTA	ATT	CTA	TGG	AAA	TGG	AAG	AAG	AAG	AAG	CGG	CCT	CGC	AAC	TCT	TAT	987	
Leu	Ile	Leu	Trp	Lys	Trp	Lys	Lys	Lys	Lys	Arg	Pro	Arg	Asn	Ser	Tyr		
265				270						275				280			
AAA	TGT	GGA	ACC	AAC	ACA	ATG	GAG	AGG	GAA	GAG	AGT	GAA	CAG	ACC	AAG	1035	
Lys	Cys	Gly	Thr	Asn	Thr	Met	Glu	Arg	Glu	Glu	Ser	Glu	Gln	Thr	Lys		
			285						290				295				
AAA	AGA	GAA	AAA	ATC	CAT	ATA	CCT	GAA	AGA	TCT	GAT	GAA	GCC	CAG	CGT	1083	
Lys	Arg	Glu	Lys	Ile	His	Ile	Pro	Glu	Arg	Ser	Asp	Glu	Ala	Gln	Arg		
			300					305					310				
GTT	TTT	AAA	AGT	TCG	AAG	ACA	TCT	TCA	TGC	GAC	AAA	AGT	GAT	ACA	TGT	1131	
Val	Phe	Lys	Ser	Ser	Lys	Thr	Ser	Ser	Cys	Asp	Lys	Ser	Asp	Thr	Cys		
		315					320					325					
TTT	TAATTA	AAGA	GTAAAG	CCCA	AAAAAA											1161	
Phe																	

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 629 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
- (A) NAME/KEY: CDS
 - (B) LOCATION: 1..96

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

AGA	AGC	TGT	TTC	AGA	AGA	AAT	GAG	GCA	AGC	AGA	GAA	ACA	AAC	AAC	AGC	48	
Arg	Ser	Cys	Phe	Arg	Arg	Asn	Glu	Ala	Ser	Arg	Glu	Thr	Asn	Asn	Ser		
1				5				10					15				

CTT ACC TTC GGG CCT GAA GAA GCA TTA GCT GAA CAG ACC GTC TTC CTT	96
Leu Thr Phe Gly Pro Glu Glu Ala Leu Ala Glu Gln Thr Val Phe Leu	
20 25 30	
TAGTTCTTCT CTGTCCATGT GGGATACATG GTATTATGTG GCTCATGAGG TACAATCTTT	156
CTTTCAGCAC CGTGCTAGCT GATCTTTCGG ACAACTTGAC ACAAGATAGA GTTAACTGGG	216
AAGAGAAAGC CTTGAATGAG GATTTCTTTC CATCAGGAAG CTACGGGCAA GTTTGCTGGG	276
CCTTTGATTG CTTGATGACT GAAGTGGAAG GGCTGAGCCC ACTGTGGGTG GTGCTAGAAA	336
TGGGCAGGGG CAGGTGACCC TGGGTGGTAT AAGAAAAAGA GCTGTCACTA AAAGGAGAGG	396
TGCCTAGTCT TACTGCAACT TGATATGTCA TGTTTGGTTG GTGTCTGTGG GAGGCCTGCC	456
CTTTTCTGAA GAGAAGTGGT GGGAGAGTGG ATGGGGTGGG GGCAGAGGAA AAGTGGGGGA	516
GAGGGCCTGG GAGGAGAGGA GGGAGGGGGA CGGGGTGGGG GTGGGGAAAA CTATGGTTGG	576
GATGTAAAAA CGGATAATAA TATAAATATT AAATAAAAAG AGAGTATTGA GCA	629

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Arg Ser Cys Phe Arg Arg Asn Glu Ala Ser Arg Glu Thr Asn Asn Ser	
1 5 10 15	
Leu Thr Phe Gly Pro Glu Glu Ala Leu Ala Glu Gln Thr Val Phe Leu	
20 25 30	

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 379 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..69

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

80

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TGC TTT GCC CCA AGA TGC AGA GAG AGA AGG AGG AAT GAG AGA TTG AGA 48
 Cys Phe Ala Pro Arg Cys Arg Glu Arg Arg Arg Asn Glu Arg Leu Arg
 1 5 10 15

AGG GAA AGT GTA CGC CCT GTA TAACAGTGTG CGCAGAAGCA AGGGGCTGAA 99
 Arg Glu Ser Val Arg Pro Val
 20

AAGATCTGAA GGTAGCCTCC GTCATCTCTT CTGGGATACA TGGATCGTGG GGATCATGAG 159

GCATTCTTCC CTTAACAAAT TTAAGCTGTT TTACCCACTA CCTCACCTTC TTA AAAACCT 219

CTTTCAGATT AAGCTGAACA GTTACAAGAT GGCTGGCATC CCTCTCCTTT CTCCCCATAT 279

GCAATTTGCT TAATGTAACC TCTTCTTTTG CCATGTTTCC ATTCTGCCAT CTTGAATTGT 339

CTTGTCAGCC AATTCATTAT CTATTAAACA CTAATTTGAG 379

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Cys Phe Ala Pro Arg Cys Arg Glu Arg Arg Arg Asn Glu Arg Leu Arg
 1 5 10 15
 Arg Glu Ser Val Arg Pro Val
 20

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 261 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..135

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

CAC AAG AAG CCG AAT CAG CCT AGC AGG CCC AGC AAC ACA GCC TCT AAG 48
 His Lys Lys Pro Asn Gln Pro Ser Arg Pro Ser Asn Thr Ala Ser Lys
 1 5 10 15

TTA GAG CGG GAT AGT AAC GCT GAC AGA GAG ACT ATC AAC CTG AAG GAA 96

81

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Leu Glu Arg Asp Ser Asn Ala Asp Arg Glu Thr Ile Asn Leu Lys Glu
 20 25 30

CTT GAA CCC CAA ATT GCT TCA GCA AAA CCA AAT GCA GAG TGAAGGCAGT 145
 Leu Glu Pro Gln Ile Ala Ser Ala Lys Pro Asn Ala Glu
 35 40 45

GAGAGCCTGA GGAAAGAGTT AAAAATTGCT TTGCCTGAAA TAAGAAGTGC AGAGTTTCTC 205

AGAATTCAAA AATGTTCTCA GCTGATTGGA ATTCTACAGT TGAATAATTA AAGAAC 261

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 45 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

His Lys Lys Pro Asn Gln Pro Ser Arg Pro Ser Asn Thr Ala Ser Lys
 1 5 10 15

Leu Glu Arg Asp Ser Asn Ala Asp Arg Glu Thr Ile Asn Leu Lys Glu
 20 25 30

Leu Glu Pro Gln Ile Ala Ser Ala Lys Pro Asn Ala Glu
 35 40 45

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 210 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 1..183

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

AAA TGG AAG AAG AAG AAG CGG CCT CGC AAC TCT TAT AAA TGT GGA ACC 48
 Lys Trp Lys Lys Lys Lys Arg Pro Arg Asn Ser Tyr Lys Cys Gly Thr
 1 5 10 15

AAC ACA ATG GAG AGG GAA GAG AGT GAA CAG ACC AAG AAA AGA GAA AAA 96
 Asn Thr Met Glu Arg Glu Glu Ser Glu Gln Thr Lys Lys Arg Glu Lys
 20 25 30

ATC CAT ATA CCT GAA AGA TCT GAT GAA GCC CAG CGT GTT TTT AAA AGT 144
 Ile His Ile Pro Glu Arg Ser Asp Glu Ala Gln Arg Val Phe Lys Ser
 35 40 45

TCG AAG ACA TCT TCA TGC GAC AAA AGT GAT ACA TGT TTT TAATTAAAGA 193
 Ser Lys Thr Ser Ser Cys Asp Lys Ser Asp Thr Cys Phe
 50 55 60

GTAAAGCCCA AAAAAAA 210

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 61 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Lys Trp Lys Lys Lys Lys Arg Pro Arg Asn Ser Tyr Lys Cys Gly Thr
 1 5 10 15

Asn Thr Met Glu Arg Glu Glu Ser Glu Gln Thr Lys Lys Arg Glu Lys
 20 25 30

Ile His Ile Pro Glu Arg Ser Asp Glu Ala Gln Arg Val Phe Lys Ser
 35 40 45

Ser Lys Thr Ser Ser Cys Asp Lys Ser Asp Thr Cys Phe
 50 55 60

(2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 359 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 249..359

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

GAGTTTTATA CCTCAATAGA CTCTTACTAG TTTCTCTTTT TCAGGTTGTG AAACCTCAACC 60

TTCAAAGACA CTCTGTTCCA TTTCTGTGGA CTAATAGGAT CATCTTTAGC ATCTGCCGGG 120

TGGATGCCAT CCAGGCTTCT TTTTCTACAT CTCTGTTTCT CGATTTTTGT GAGCCTAGGA 180

GGTGCCTAAG CTCCATTGGC TCTAGATTCC TGGCTTTCCC CATCATGTTC TCCAAAGCAT 240

CTGAAGCT ATG GCT TGC AAT TGT CAG TTG ATG CAG GAT ACA CCA CTC CTC 290
 Met Ala Cys Asn Cys Gln Leu Met Gln Asp Thr Pro Leu Leu
 1 5 10

AAG TTT CCA TGT CCA AGG CTC AAT CTT CTC TTT GTG CTG CTG ATT CGT 338
 Lys Phe Pro Cys Pro Arg Leu Asn Leu Leu Phe Val Leu Leu Ile Arg
 15 20 25 30

CTT TCA CAA GTG TCT TCA GAT 359
 Leu Ser Gln Val Ser Ser Asp
 35

(2) INFORMATION FOR SEQ ID NO:34:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 37 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Met Ala Cys Asn Cys Gln Leu Met Gln Asp Thr Pro Leu Leu Lys Phe
 1 5 10 15

Pro Cys Pro Arg Leu Ile Leu Leu Phe Val Leu Leu Ile Arg Leu Ser
 20 25 30

Gln Val Ser Ser Asp
 35

(2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 416 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 318..416

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

CCAAAGAAAA AGTGATTTGT CATTGCTTTA TAGACTGTAA GAAGAGAACA TCTCAGAAGT 60

GGAGTCTTAC CCTGAAATCA AAGGATTTAA AGAAAAAGTG GAATTTTCT TCAGCAAGCT 120

GTGAACTAA ATCCACAACC TTTGGAGACC CAGGAACACC CTCCAATCTC TGTGTGTTTT 180
 GTAAACATCA CTGGAGGGTC TTCTACGTGA GCAATTGGAT TGTCATCAGC CCTGCCTGTT 240
 TTGCACCTGG GAAGTGCCCT GGTCTTACTT GGGTCCAAAT TGTGGCTTT CACTTTTGAC 300
 CCTAAGCATC TGAAGCC ATG GGC CAC ACA CGG AGG CAG GGA ACA TCA CCA 350
 Met Gly His Thr Arg Arg Gln Gly Thr Ser Pro
 1 5 10
 TCC AAG TGT CCA TAC CTG AAT TTC TTT CAG CTC TTG GTG CTG GCT GGT 398
 Ser Lys Cys Pro Tyr Leu Asn Phe Phe Gln Leu Leu Val Leu Ala Gly
 15 20 25
 CTT TCT CAC TTC TGT TCA 416
 Leu Ser His Phe Cys Ser
 30

(2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 33 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Met Gly His Thr Arg Arg Gln Gly Thr Ser Pro Ser Lys Cys Pro Tyr
 1 5 10 15
 Leu Asn Phe Phe Gln Leu Leu Val Leu Ala Gly Leu Ser His Phe Cys
 20 25 30
 Ser

(2) INFORMATION FOR SEQ ID NO:37:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 113 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 99..113

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

GGAGCAAGCA GACGCGTAAG AGTGGCTCCT GTAGGCAGCA CGGACTTGAA CAACCAGACT 60

85

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CCTGTAGACG TGTTCCAGAA CTTACGGAAG CACCCACG ATG GAC CCC AGA TGC 113
 Met Asp Pro Arg Cys
 1 5

(2) INFORMATION FOR SEQ ID NO:38:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 5 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

Met Asp Pro Arg Cys
 1 5

(2) INFORMATION FOR SEQ ID NO:39:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 124 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 107..124

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

CACAGGGTGA AAGCTTTGCT TCTCTGCTGC TGTAACAGGG ACTAGCACAG ACACACGGAT 60

GAGTGGGGTC ATTTCCAGAT ATTAGGTCAC AGCAGAAGCA GCCAAA ATG GAT CCC 115
 Met Asp Pro
 1

CAG TGC ACT 124
 Gln Cys Thr
 5

(2) INFORMATION FOR SEQ ID NO:40:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

86

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

Met Asp Pro Gln Cys Thr
 1 5

(2) INFORMATION FOR SEQ ID NO:41:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 195 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
 (B) LOCATION: 148..195

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

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AGGAGCCTTA GGAGGTACGG GGAGCTCGCA AATACTCCTT TTGGTTTATT CTTACCACCT      60
TGCTTCTGTG TTCCTTGGA ATGCTGCTGT GCTTATGCAT CTGGTCTCTT TTTGGAGCTA      120
CAGTGGACAG GCATTTGTGA CAGCACT ATG GGA CTG AGT AAC ATT CTC TTT          171
                  Met Gly Leu Ser Asn Ile Leu Phe
                  1 5
GTG ATG GCC TTC CTG CTC TCT GGT          195
Val Met Ala Phe Leu Leu Ser Gly
    10 15

```

(2) INFORMATION FOR SEQ ID NO:42:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 16 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

```

Met Gly Leu Ser Asn Ile Leu Phe Val Met Ala Phe Leu Leu Ser Gly
  1 5 10 15

```

(2) INFORMATION FOR SEQ ID NO: 43:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 22 base pairs

87

A

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

CCAACATAAC TGAGTCTGGA AA

22

(2) INFORMATION FOR SEQ ID NO: 44:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:

CTGGATTCTG ACTCACCTTC A

21

(2) INFORMATION FOR SEQ ID NO: 45:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:

AGGTTAAGAG TGGTAGAGCC A

21

(2) INFORMATION FOR SEQ ID NO: 46:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:

AATACCATGT ATCCACATG G

21

(2) INFORMATION FOR SEQ ID NO: 47:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:

CTGAAGCTAT GGCTTGCAAT T

21

(2) INFORMATION FOR SEQ ID NO: 48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:

TGGCTTCTCT TTCCTTACCT T

21

(2) INFORMATION FOR SEQ ID NO: 49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49:

GCAAATGGTA GATGAGACTG T

21

(2) INFORMATION FOR SEQ ID NO: 50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50:

CAACCGAGAA ATCTACCACT AA

22

(2) INFORMATION FOR SEQ ID NO: 51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51:

GCCGGTAACA AGTCTCTTCA

20

(2) INFORMATION FOR SEQ ID NO: 52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 52:

AAAAGCTCTA TAGCATTCTG TC

22

(2) INFORMATION FOR SEQ ID NO: 53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53:

ACTGACTTGG ACAGTTGTTC A

21

(2) INFORMATION FOR SEQ ID NO: 54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 54:

TTTGATGGAC AACTTTACTA

20

(2) INFORMATION FOR SEQ ID NO: 55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 55:
CAGCTCACTC AGGCTTATGT 20

(2) INFORMATION FOR SEQ ID NO: 56:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 21 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 56:
AAACAGCATC TGAGATCAGC A 21

(2) INFORMATION FOR SEQ ID NO: 57:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 57:
CTGAGATCAG CAAGACTGTC 20

(2) INFORMATION FOR SEQ ID NO: 58:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 21 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 58:
CTGAAGCTAT GGCTTGCAAT T 21

(2) INFORMATION FOR SEQ ID NO: 59:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 22 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 59:

ACAAGTGTCT TCAGATGTTG AT

22

(2) INFORMATION FOR SEQ ID NO: 60:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 60:

CTGGATTCTG ACTCACCTTC A

21

(2) INFORMATION FOR SEQ ID NO: 61:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 61:

CCAGGTGAAG TCCTCTGACA

20

(2) INFORMATION FOR SEQ ID NO:62:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1417 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 249..884

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

GAGTTTTATA CCTCAATAGA CTCTTACTAG TTTCTCTTTT TCAGGTTGTG AAACCTCAACC

60

TTCAAAGACA CTCTGTTCCA TTTCTGTGGA CTAATAGGAT CATCTTTAGC ATCTGCCGGG

120

TGGATGCCAT CCAGGCTTCT TTTTCTACAT CTCTGTTTCT CGATTTTGT GAGCCTAGGA

180

GGTGCCTAAG CTCCATTGGC TCTAGATTCC TGGCTTTCCC CATCATGTTC TCCAAAGCAT

240

CTGAAGCT ATG GCT TGC AAT TGT CAG TTG ATG CAG GAT ACA CCA CTC CTC

290

Met Ala Cys Asn Cys Gln Leu Met Gln Asp Thr Pro Leu Leu

1

5

10

92

A

AAG TTT CCA TGT CCA AGG CTC AAT CTT CTC TTT GTG CTG CTG ATT CGT	338
Lys Phe Pro Cys Pro Arg Leu Asn Leu Leu Phe Val Leu Leu Ile Arg	
15 20 25 30	
CTT TCA CAA GTG TCT TCA GAT GTT GAT GAA CAA CTG TCC AAG TCA GTG	386
Leu Ser Gln Val Ser Ser Asp Val Asp Glu Gln Leu Ser Lys Ser Val	
35 40 45	
AAA GAT AAG GTA TTG CTG CCT TGC CGT TAC AAC TCT CCT CAT GAA GAT	434
Lys Asp Lys Val Leu Leu Pro Cys Arg Tyr Asn Ser Pro His Glu Asp	
50 55 60	
GAG TCT GAA GAC CGA ATC TAC TGG CAA AAA CAT GAC AAA GTG GTG CTG	482
Glu Ser Glu Asp Arg Ile Tyr Trp Gln Lys His Asp Lys Val Val Leu	
65 70 75	
TCT GTC ATT GCT GGG AAA CTA AAA GTG TGG CCC GAG TAT AAG AAC CGG	530
Ser Val Ile Ala Gly Lys Leu Lys Val Trp Pro Glu Tyr Lys Asn Arg	
80 85 90	
ACT TTA TAT GAC AAC ACT ACC TAC TCT CTT ATC ATC CTG GGC CTG GTC	578
Thr Leu Tyr Asp Asn Thr Thr Tyr Ser Leu Ile Ile Leu Gly Leu Val	
95 100 105 110	
CTT TCA GAC CGG GGC ACA TAC AGC TGT GTC GTT CAA AAG AAG GAA AGA	626
Leu Ser Asp Arg Gly Thr Tyr Ser Cys Val Val Gln Lys Lys Glu Arg	
115 120 125	
GGA ACG TAT GAA GTT AAA CAC TTG GCT TTA GTA AAG TTG TCC ATC AAA	674
Gly Thr Tyr Glu Val Lys His Leu Ala Leu Val Lys Leu Ser Ile Lys	
130 135 140	
CCC CCA GAA GAC CCT CCT GAT AGC AAG AAC ACA CTT GTG CTC TTT GGG	722
Pro Pro Glu Asp Pro Pro Asp Ser Lys Asn Thr Leu Val Leu Phe Gly	
145 150 155	
GCA GGA TTC GGC GCA GTA ATA ACA GTC GTC GTC ATC GTT GTC ATC ATC	770
Ala Gly Phe Gly Ala Val Ile Thr Val Val Val Ile Val Val Ile Ile	
160 165 170	
AAA TGC TTC TGT AAG CAC AGA AGC TGT TTC AGA AGA AAT GAG GCA AGC	818
Lys Cys Phe Cys Lys His Arg Ser Cys Phe Arg Arg Asn Glu Ala Ser	
175 180 185 190	
AGA GAA ACA AAC AAC AGC CTT ACC TTC GGG CCT GAA GAA GCA TTA GCT	866
Arg Glu Thr Asn Asn Ser Leu Thr Phe Gly Pro Glu Glu Ala Leu Ala	
195 200 205	
GAA CAG ACC GTC TTC CTT TAGTTCTTCT CTGTCCATGT GGGATACATG GTATTATGTG	924
Glu Gln Thr Val Phe Leu	
210	
GCTCATGAGG TACAATCTTT CTTTCAGCAC CGTGCTAGCT GATCTTTCGG ACAACTTGAC	984
ACAAGATAGA GTTAACTGGG AAGAGAAAGC CTTGAATGAG GATTTCTTTC CATCAGGAAG	1044
CTACGGGCAA GTTTGCTGGG CCTTTGATTG CTTGATGACT GAAGTGGAAG GGCTGAGCCC	1104

ACTGTGGGTG GTGCTAGCCC TGGGCAGGGG CAGGTGACCC TGGGTGGTAT AAGAAAAAGA 1164
 GCTGTCACTA AAAGGAGAGG TGCCTAGTCT TACTGCAACT TGATATGTCA TGTTTGTTG 1224
 GTGTCTGTGG GAGGCCTGCC CTTTCTGAA GAGAAGTGGT GGGAGAGTGG ATGGGGTGGG 1284
 GGCAGAGGAA AAGTGGGGGA GAGGGCCTGG GAGGAGAGGA GGGAGGGGGA CGGGGTGGGG 1344
 GTGGGGAAAA CTATGGTTGG GATGTAAAAA CGGATAATAA TATAAATATT AAATAAAAAG 1404
 AGAGTATTGA GCA 1417

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 212 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

Met	Ala	Cys	Asn	Cys	Gln	Leu	Met	Gln	Asp	Thr	Pro	Leu	Leu	Lys	Phe	1	5	10	15
Pro	Cys	Pro	Arg	Leu	Ile	Leu	Leu	Phe	Val	Leu	Leu	Ile	Arg	Leu	Ser	20	25	30	
Gln	Val	Ser	Ser	Asp	Val	Asp	Glu	Gln	Leu	Ser	Lys	Ser	Val	Lys	Asp	35	40	45	
Lys	Val	Leu	Leu	Pro	Cys	Arg	Tyr	Asn	Ser	Pro	His	Glu	Asp	Glu	Ser	50	55	60	
Glu	Asp	Arg	Ile	Tyr	Trp	Gln	Lys	His	Asp	Lys	Val	Val	Leu	Ser	Val	65	70	75	80
Ile	Ala	Gly	Lys	Leu	Lys	Val	Trp	Pro	Glu	Tyr	Lys	Asn	Arg	Thr	Leu	85	90	95	
Tyr	Asp	Asn	Thr	Thr	Tyr	Ser	Leu	Ile	Ile	Leu	Gly	Leu	Val	Leu	Ser	100	105	110	
Asp	Arg	Gly	Thr	Tyr	Ser	Cys	Val	Val	Gln	Lys	Lys	Glu	Arg	Gly	Thr	115	120	125	
Tyr	Glu	Val	Lys	His	Leu	Ala	Leu	Val	Lys	Leu	Ser	Ile	Lys	Pro	Pro	130	135	140	
Glu	Asp	Pro	Pro	Asp	Ser	Lys	Asn	Thr	Leu	Val	Leu	Phe	Gly	Ala	Gly	145	150	155	160
Phe	Gly	Ala	Val	Ile	Thr	Val	Val	Val	Ile	Val	Val	Ile	Ile	Lys	Cys	165	170	175	
Phe	Cys	Lys	His	Arg	Ser	Cys	Phe	Arg	Arg	Asn	Glu	Ala	Ser	Arg	Glu	180	185	190	

Thr Asn Asn Ser Leu Thr Phe Gly Pro Glu Glu Ala Leu Ala Glu Gln
 195 200 205

Thr Val Phe Leu
 210

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1606 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 249..926

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

GAGTTTATA CCTCAATAGA CTCTTACTAG TTTCTCTTTT TCAGGTTGTG AACTCAACC	60
TTCAAAGACA CTCTGTTCCA TTTCTGTGGA CTAATAGGAT CATCTTTAGC ATCTGCCGGG	120
TGGATGCCAT CCAGGCTTCT TTTTCTACAT CTCTGTTTCT CGATTTTGTG GAGCCTAGGA	180
GGTGCCTAAG CTCCATTGGC TCTAGATTCC TGGCTTTCCC CATCATGTTC TCAAAGCAT	240
CTGAAGCT ATG GCT TGC AAT TGT CAG TTG ATG CAG GAT ACA CCA CTC CTC	290
Met Ala Cys Asn Cys Gln Leu Met Gln Asp Thr Pro Leu Leu	
1 5 10	
AAG TTT CCA TGT CCA AGG CTC AAT CTT CTC TTT GTG CTG CTG ATT CGT	338
Lys Phe Pro Cys Pro Arg Leu Asn Leu Leu Phe Val Leu Leu Ile Arg	
15 20 25 30	
CTT TCA CAA GTG TCT TCA GAT GTT GAT GAA CAA CTG TCC AAG TCA GTG	386
Leu Ser Gln Val Ser Ser Asp Val Asp Glu Gln Leu Ser Lys Ser Val	
35 40 45	
AAA GAT AAG GTA TTG CTG CCT TGC CGT TAC AAC TCT CCT CAT GAA GAT	434
Lys Asp Lys Val Leu Leu Pro Cys Arg Tyr Asn Ser Pro His Glu Asp	
50 55 60	
GAG TCT GAA GAC CGA ATC TAC TGG CAA AAA CAT GAC AAA GTG GTG CTG	482
Glu Ser Glu Asp Arg Ile Tyr Trp Gln Lys His Asp Lys Val Val Leu	
65 70 75	
TCT GTC ATT GCT GGG AAA CTA AAA GTG TGG CCC GAG TAT AAG AAC CGG	530
Ser Val Ile Ala Gly Lys Leu Lys Val Trp Pro Glu Tyr Lys Asn Arg	
80 85 90	
ACT TTA TAT GAC AAC ACT ACC TAC TCT CTT ATC ATC CTG GGC CTG GTC	578

Thr	Leu	Tyr	Asp	Asn	Thr	Thr	Tyr	Ser	Leu	Ile	Ile	Leu	Gly	Leu	Val		
95					100					105					110		
CTT	TCA	GAC	CGG	GGC	ACA	TAC	AGC	TGT	GTC	GTT	CAA	AAG	AAG	GAA	AGA	626	
Leu	Ser	Asp	Arg	Gly	Thr	Tyr	Ser	Cys	Val	Val	Gln	Lys	Lys	Glu	Arg		
				115					120					125			
GGA	ACG	TAT	GAA	GTT	AAA	CAC	TTG	GCT	TTA	GTA	AAG	TTG	TCC	ATC	AAA	674	
Gly	Thr	Tyr	Glu	Val	Lys	His	Leu	Ala	Leu	Val	Lys	Leu	Ser	Ile	Lys		
			130					135					140				
CCC	CCA	GAA	GAC	CCT	CCT	GAT	AGC	AAG	AAC	ACA	CTT	GTG	CTC	TTT	GGG	722	
Pro	Pro	Glu	Asp	Pro	Pro	Asp	Ser	Lys	Asn	Thr	Leu	Val	Leu	Phe	Gly		
			145				150						155				
GCA	GGA	TTC	GGC	GCA	GTA	ATA	ACA	GTC	GTC	GTC	ATC	GTT	GTC	ATC	ATC	770	
Ala	Gly	Phe	Gly	Ala	Val	Ile	Thr	Val	Val	Val	Ile	Val	Val	Ile	Ile		
	160					165					170						
AAA	TGC	TTC	TGT	AAG	CAC	GGT	CTC	ATC	TAC	CAT	TTG	CAA	CTG	ACC	TCT	818	
Lys	Cys	Phe	Cys	Lys	His	Gly	Leu	Ile	Tyr	His	Leu	Gln	Leu	Thr	Ser		
175					180				185					190			
TCT	GCA	AAG	GAC	TTC	AGA	AAC	CTA	GCA	CTA	CCC	TGG	CTC	TGC	AAA	CAC	866	
Ser	Ala	Lys	Asp	Phe	Arg	Asn	Leu	Ala	Leu	Pro	Trp	Leu	Cys	Lys	His		
				195				200					205				
GGT	TCT	CTA	GGT	GAA	GCC	TCT	GCA	GTG	ATT	TGC	AGA	AGT	ACT	CAG	ACG	914	
Gly	Ser	Leu	Gly	Glu	Ala	Ser	Ala	Val	Ile	Cys	Arg	Ser	Thr	Gln	Thr		
			210					215					220				
AAT	GAA	CCA	CAG	TAGTTCTGCT	GTTTCTGAGG	ACGTAGTTTA	GAGACTGAAT									966	
Asn	Glu	Pro	Gln														
			225														
TCTTTGGAAA	GGACATAGGG	ACAGTTTGCA	CATTTGCTTG	CACATCACAC	ACACACACAC											1026	
ACACACACAC	ACACACACAC	ACACACACAC	ACACACACAC	ACACACACAC	ACACACACAC	TCTCTCTCTC										1086	
TCTCTCTCTC	GATACCTTAG	GATAGGGTTC	TACCCTGTTG	CTCAGTGACA	AAGAATCACT											1146	
CTGTGGCGGA	GGCAGGCTTC	AAGCTTGCAG	CAATCCTCCT	GCACCAGTTT	CCTGAGTGCC											1206	
AGACTTCCAG	GTGTAAGCTA	TGGCACTTAG	CAGAACACTA	GCTGAATCAA	TGAAGACACT											1266	
GAGGTTCCAA	GAGGGAACCT	GAATTATGAA	GGTGAGTCAG	AATCCAGATT	TCCTGGCTCT											1326	
ACCACTCTTA	ACCTGTATCT	GTTAGACCCC	AAGCTCTGAG	CTCATAGACA	AGCTAATTTA											1386	
AAATGCTTTT	TAATAAGCAG	AAGGCTCAGT	TAGTACGGGG	TTCAGGATAC	TGCTTACTGG											1446	
CAATATTTGA	CTAGCCTCTA	TTTTGTTTGT	TTTTTAAAGG	CCTACTGACT	GTAGTGTAAT											1506	
TTGTAGGAAA	CATGTTGCTA	TGTATACCCA	TTTGAGGGTA	ATAAAAAATGT	TGGTAATTTT											1566	
CAGCCAGCAC	TTTCCAGGTA	TTTCCCTTTT	TATCCTTCAT													1606	

(2) INFORMATION FOR SEQ ID NO:65:

96

A

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 226 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

Met Ala Cys Asn Cys Gln Leu Met Gln Asp Thr Pro Leu Leu Lys Phe
 1 5 10 15

Pro Cys Pro Arg Leu Ile Leu Leu Phe Val Leu Leu Ile Arg Leu Ser
 20 25 30

Gln Val Ser Ser Asp Val Asp Glu Gln Leu Ser Lys Ser Val Lys Asp
 35 40 45

Lys Val Leu Leu Pro Cys Arg Tyr Asn Ser Pro His Glu Asp Glu Ser
 50 55 60

Glu Asp Arg Ile Tyr Trp Gln Lys His Asp Lys Val Val Leu Ser Val
 65 70 75 80

Ile Ala Gly Lys Leu Lys Val Trp Pro Glu Tyr Lys Asn Arg Thr Leu
 85 90 95

Tyr Asp Asn Thr Thr Tyr Ser Leu Ile Ile Leu Gly Leu Val Leu Ser
 100 105 110

Asp Arg Gly Thr Tyr Ser Cys Val Val Gln Lys Lys Glu Arg Gly Thr
 115 120 125

Tyr Glu Val Lys His Leu Ala Leu Val Lys Leu Ser Ile Lys Pro Pro
 130 135 140

Glu Asp Pro Pro Asp Ser Lys Asn Thr Leu Val Leu Phe Gly Ala Gly
 145 150 155 160

Phe Gly Ala Val Ile Thr Val Val Val Ile Val Val Ile Ile Lys Cys
 165 170 175

Phe Cys Lys His Gly Leu Ile Tyr His Leu Gln Leu Thr Ser Ser Ala
 180 185 190

Lys Asp Phe Arg Asn Leu Ala Leu Pro Trp Leu Cys Lys His Gly Ser
 195 200 205

Leu Gly Glu Ala Ser Ala Val Ile Cys Arg Ser Thr Gln Thr Asn Glu
 210 215 220

Pro Gln
 225